

☒ Drafts

☒ Pending

☒ Active

☒ Failed

☒ Saved

☒ S1: (162) KATO-SEISHI.in. SEKINE-SHINGO.in. SEKINE-SHINGO-NISHIOONUNA.in. YAMAGUCHI-TOMOKI.in. YA...

☒ S2: (18932) 530/350.ccls.

☒ S3: (10) S1 and S2

☒ S5: (162) KATO-SEISHI.in. SEKINE-SHINGO.in. SEKINE-SHINGO-NISHIOONUNA.in. YAMAGUCHI-TOMOKI.in. YA...

☒ S6: (5) S4 and S5

☒ S4: (3902) TM4

☒ S8: (18465) 530/350.ccls.

☒ S9: (9) S5 and S8

☒ S11: (1) "6054289".pr

☒ Favorites

☒ Tagged (1)

☒ UDC

☒ Queue

☒ Trash

EAST Search 4/5/06
P116

BEST AVAILABLE COPY

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:31:55 ; Search time 7.5 Seconds
(without alignments)
1673.356 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atgggccagcgccatcac.....tccactggcggaacctatgca 759

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 1144120

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlip
-Q=/abss/ABSSWEB.spool/US10608388/runat_04042006_150655_14135/app.query.fasta_1
-DB=Issued Patents AA -QPM=fastan -SUFFIX=n2p.ra1 -MINMATCH=0.1 -LOOPCL=0
-LDOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFWT=pct -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=2000000000
-HOST=abs02p -USER=US10608388 -CGN 1 1 71 -runat_04042006_150655_14135
-NCPU=6 -ICPU=3 -NO_MMAP -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Issued Patents AA.*
1: /cgn2_6/ptodata/1/iaa/5_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/6_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/H_COMB.pep.*
4: /cgn2_6/ptodata/1/iaa/PTCUS_COMB.pep.*
5: /cgn2_6/ptodata/1/iaa/RE_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1300	91.0	252	2	US-08-705-771-17
2	1300	91.0	252	2	US-09-417-540-17
3	453	31.7	222	2	US-10-037-417-81
4	344	24.1	253	2	US-09-333-599-4
5	344	24.1	253	2	US-09-499-781-4
6	343.5	24.0	249	2	US-09-949-016-8334
7	333.5	23.3	267	2	US-09-949-016-9088
8	333.5	23.3	275	2	US-09-949-016-8346
9	332	23.2	253	2	US-09-333-599-2
10	332	23.2	253	2	US-09-499-781-2
11	332	23.2	276	2	US-09-949-016-8972
12	329	23.0	245	2	US-10-012-231A-4

13	329	23.0	245	2	US-10-015-389A-4	Sequence 4, Appli
14	329	23.0	245	2	US-10-006-768A-4	Sequence 4, Appli
15	329	23.0	245	2	US-10-015-671A-4	Sequence 4, Appli
16	329	23.0	245	2	US-10-015-393A-4	Sequence 4, Appli
17	329	23.0	245	2	US-10-011-833A-4	Sequence 4, Appli
18	329	23.0	245	2	US-10-006-041A-4	Sequence 4, Appli
19	329	23.0	245	2	US-10-012-064A-4	Sequence 4, Appli
20	303	21.2	255	2	US-09-949-016-9861	Sequence 9861, Ap
21	301.5	21.1	238	2	US-09-949-016-6334	Sequence 6334, Ap
22	299.5	21.0	222	2	US-09-949-016-8347	Sequence 8347, Ap
23	297.5	20.8	260	2	US-09-949-016-7296	Sequence 7296, Ap
24	297.5	20.8	270	2	US-09-949-016-9117	Sequence 9117, Ap
25	285	19.9	265	1	US-08-807-044-1	Sequence 1, Appli
26	283	19.8	267	2	US-08-430-225A-20	Sequence 20, Appl
27	283	19.8	267	2	US-09-795-380-20	Sequence 20, Appl
28	273.5	19.1	219	1	US-08-855-140-3	Sequence 3, Appli
29	273.5	19.1	219	1	US-08-807-044-3	Sequence 3, Appli
30	273.5	19.1	219	4	PCT-US91-04986-2	Sequence 2, Appli
31	273.5	19.1	231	2	US-09-949-016-10626	Sequence 10626, A
32	271	19.0	280	1	US-08-855-140-1	Sequence 1, Appli
33	270.5	18.9	219	1	US-08-855-140-4	Sequence 1, Appli
34	263	18.4	241	2	US-08-808-148-1	Sequence 1, Appli
35	263	18.4	241	2	US-09-020-956-114	Sequence 114, App
36	263	18.4	241	2	US-09-030-607-114	Sequence 114, App
37	263	18.4	241	2	US-09-439-313-114	Sequence 114, App
38	263	18.4	241	2	US-09-352-616A-114	Sequence 114, App
39	263	18.4	241	2	US-09-232-149A-114	Sequence 114, App
40	263	18.4	241	2	US-09-159-812-114	Sequence 114, App
41	263	18.4	241	2	US-09-636-215-114	Sequence 114, App
42	263	18.4	241	2	US-09-685-166A-114	Sequence 114, App
43	263	18.4	241	2	US-09-115-453-114	Sequence 114, App
44	263	18.4	241	2	US-09-688-489-114	Sequence 114, App
45	263	18.4	241	2	US-09-679-426-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-08-705-771-17
Sequence 17, Application US/08705771
Patent No. 6054289

GENERAL INFORMATION:
APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
APPLICANT: Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
TITLE OF INVENTION: Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/705,771
FILING DATE: August 30, 1996
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:

LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-705-771-17

Alignment Scores:

Pred. No.:	4,65e-138	Length:	252
Score:	1300.00	Matches:	252
Percent Similarity:	98.8%	Conservative:	0
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	91.0%	Indels:	3
DB:	2	Gaps:	0

US-10-608-388A-1 (1-759) x US-08-705-771-17 (1-252)

```
QY 1 ATGGGCGGAGTGGGCGATCACCTCTCCAGACCGTGGTCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGGAGCTGGGCTTTTATGCTATGTGGAGCGCTATGCTTCATCACTTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTGAAGATGTGTACACGCTCATCCCTGCTAGTGTATGATCATCTGTA 180
DB 41 TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCGCTCTCTTTTATCATCTGGGCTAATGGCTGTGTGCCACCAATCGGGAAGTGGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGGCAGCTGTTGTATCATCTCTGCTCTCTGTTTGTTCACAGAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GNGGTTTGGGATATCTTTACAGACCAAGTGGAAATGAGTTGATCGCAGCATTTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGATATAGACCTTACAAATGGACCAACCTGTATGCTGTAGCGGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACACAGCTGATTTGTGGAATTCACACTCTCAGACTCAGCTGGGAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACCAAGACGAGTGCCCTCTAGCTGTGACAGAGACTGCCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysArgGluThrAlaSer 180
QY 541 AATTGTATAGGCGAGCTGGCCCAACCTCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySer-Trip-ProProPheArg-LeuTyrAlaGluGlyCysGluAlaLeu 199
QY 601 GTAGTGAAGAGCTACAGAAATCATGATGCTATGATCTGGCCCGCAGCTGCATTGCA 660
DB 200 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 219
QY 661 GCTATTACGCTCTGGGCTGCTGTGCTGTCTCATCTGCTGTGCGAAGAGGATGAGAT 720
DB 220 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 739
QY 721 CCTGCTTACGAGCTCTCATCTACTGCGGAACCTATGCA 759
DB 240 ProIaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 252
```

RESULT 2

US-09-417-540-17

Sequence 17, Application US/09417540

Patent No. 6639052

GENERAL INFORMATION:

APPLICANT: Paul Moore, Reiner Gentz, Hongjin Ji,
Jian Ni and Jing-Shan Hu
TITLE OF INVENTION: Human Genes, Sequences and
Expression Products
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
STREET: 6 BECKER FARM ROAD
CITY: ROSELAND
STATE: NEW JERSEY
COUNTRY: USA
ZIP: 07068
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH DISKETTE
COMPUTER: IBM PS/2
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/417,540
FILING DATE: 14-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/705,771
FILING DATE: August 30, 1996
ATTORNEY/AGENT INFORMATION:
NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 325800-346 (PF196)
TELECOMMUNICATION INFORMATION:
TELEPHONE: 973-994-1700
TELEFAX: 973-994-1744
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 252 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 17:
US-09-417-540-17

Alignment Scores:

Pred. No.:	4,65e-138	Length:	252
Score:	1300.00	Matches:	252
Percent Similarity:	98.8%	Conservative:	0
Best Local Similarity:	98.8%	Mismatches:	0
Query Match:	91.0%	Indels:	3
DB:	2	Gaps:	0

US-10-608-388A-1 (1-759) x US-09-417-540-17 (1-252)

```
QY 1 ATGGGCGGAGTGGGCGATCACCTCTCCAGACCGTGGTCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGGAGCTGGGCTTTTATGCTATGTGGAGCGCTATGCTTCATCACTTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTGAAGATGTGTACACGCTCATCCCTGCTAGTGTATGATCATCTGTA 180
DB 41 TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCGCTCTCTTTTATCATCTGGGCTAATGGCTGTGTGCCACCAATCGGGAAGTGGC 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGGCAGCTTGTGTATCATCTCTGCTCTGTTTGTTCACAGAGTGTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGACCAAGTGGAAATGAGTTGATCGCAGCATTTCAG 360
```



```
QY 427 AGACAGCTGATGTTGGATTTCAACAATCTACAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysGlySerAsnAsnSerGlnAspTrpGlnAspSerGluTrpIle 170
QY 487 AAA-----GAACCAAAACACAGAGTGTCCCTTGTAGCTGTGCAGAGACTGCCAGC 540
Db 171 ArgSerGlyGluAlaAspSerArgValValProAspSerCysGlySerMetValAla 190
QY 541 AATTGTAATGGCAGCTGGCCACCTTCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 GlyCys---GlyLysArgAspHisAlaSerAsnIleTrpLysValGluGlyGlyCysIle 209
QY 595 GCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATGATGATGATGATGATGATGATG 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTTGACGCTATTGAGCTGTGGGCTGCTGTGTGTGCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 6
US-09-949-016-8334
; Sequence 8334, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; PRIOR FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8334
; LENGTH: 249
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8334

Alignment Scores:
Pred. No.: 5,36e-30 Length: 249
Score: 343.50 Matches: 85
Percent Similarity: 50.2% Conservative: 41
Best Local Similarity: 33.9% Mismatches: 102
Query Match: 24.0% Indels: 23
DB: 2 Gaps: 7

US-10-608-388A-1 (1-759) x US-09-949-016-8334 (1-249)
QY 16 ATCACTCTCCAGACCGTGTGGTCTTCTCAACCTCATCTTCTGGGGGAGCTGGC 75
Db 12 IleThrCysLeuLysThrLeuLeuIleIleTyrSerPheValPheTrpIleThrGlyVal 31
QY 76 ATTTATGCTATGTGGAGCGCTATGCTTCATCATCATATGATGACATGACCATCTCTTT 135
Db 32 IleLeuLeuAlaValGlyValTrpGlyLysLeuThrLeuGlyThrTyrIleSerLeuIle 51
QY 136 GAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATGCTGTAGAGCCCTGCTTTTC 195
Db 52 AlaGluAsnSerThrAsnAlaPro---TyrValLeuIleGlyThrGlyThrThrIleVal 70
QY 196 ATCATTTGGCTAATTGGCTGTGCGCAATCCGGGAAGTCGCTGTGAGATTGCCAGC 255
Db 71 ValPheGlyLeuPheGlyCysPheAlaThrCysArgGlySerProTrpMetLeuLysLeu 90
QY 256 TTTGTTCATCATCTGCTCTGTGTTTGTGTCACAGAGTTGTGTAGTGGTTTGGGATAT 315
Db 36 IleThrCysPheLysSerValLeuLeuIleTyrThrPheIlePheTrpIleThrGlyVal 55
```

```
Db 91 TyrAlaMetPheLeuSerLeuValPheLeuAlaGluLeuValAlaGlyIleSerGlyPhe 110
QY 316 GTTTACAGAGCAAAAGTGGAAAATAGGTTGATCGCAGCATTCAGAAAGTGTATAAGACC 375
Db 111 ValPheArgHisGluIleLysAspThrPheLeuArgThrTyrThrAspAlaMetGlnThr 130
QY 376 TACAATGGAAACCAACCTCATGCTGCTAGCGGGCTATTGATTATGTACAGACACAGCTG 435
Db 131 TyrAsnGlyAsn-----AspGluArgSerArgAlaValAspHisValGlnArgSerLeu 148
QY 436 CATTTGTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTCAAAGAAACC 495
Db 149 SerCysCysGlyValGlnAsnTyrThrAsnTrpSerThrSerProTyrPheLeuGlu--- 167
QY 496 AAAAACCCAGAGTGTCCCTCTTAGCTGCTGCAGAGAGACTGCCAGCAATGTATGGCAGC 555
Db 168 -----HisGlyIleProProSerCysCysMet---AsnGluThrAspCysAsn----- 182
QY 556 CTGGCCCACTTCGACCTCTAT-----GCTGAG 585
Db 183 -----ProGlnAspLeuHisAsnLeuThrValAlaAlaThrLysValAsnGlnLys 199
QY 586 GGGTGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATGATGATGATGATG 645
Db 200 GlyCysTyrAspLeuValThrSerPheMetGluThrAsnMetGlyIleIleAlaGlyVal 219
QY 646 GCACTGGCAATTGCGAGCTATTACAGCTGTGGGCACTGCTGTGCTGCTGCTGCTGCTG 705
Db 220 AlaPheGlyIleAlaPheSerGlnLeuIleGlyMetLeuLeuAlaCys---CysLeuSer 238
QY 706 AGAAGAGTAGAGATCCTGCTTACGAGCTCCTC 738
Db 239 ArgPheIleThrAlaAsnGlnTyrGluMetVal 249

RESULT 7
US-09-949-016-9088
; Sequence 9088, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 9088
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9088

Alignment Scores:
Pred. No.: 7,43e-29 Length: 267
Score: 333.50 Matches: 78
Percent Similarity: 50.0% Conservative: 46
Best Local Similarity: 31.5% Mismatches: 101
Query Match: 23.3% Indels: 23
DB: 2 Gaps: 6

US-10-608-388A-1 (1-759) x US-09-949-016-9088 (1-267)
QY 16 ATCACTCTCCAGACCGTGTGGTCTTCTCAACCTCATCTTCTGGGGGAGCTGGC 75
Db 36 IleThrCysPheLysSerValLeuLeuIleTyrThrPheIlePheTrpIleThrGlyVal 55
```


; CURRENT APPLICATION NUMBER: US/09/333,599
; CURRENT FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-333-599-2

Alignment Scores:
Pred. No.: 1.07e-28 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservatives: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 2 Gaps: 4

US-10-608-388A-1 (1-759) x US-09-333-599-2 (1-253)

```
QY 10 TGGGGCATACCTCTCCAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 GCTGGCATTTATGCTATGTGGAGCGCTATGCTTTCATCACTTATGATGACTATGACCAC 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 TTCTTTGAAGATGTATACCGCTCATCCCTGCTGTAGTATCATATGCTGTAGGAGCCCTG 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValAlaGlyThrVal 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 CTTTTCATCATGGCTAAATGGCTGTGCGCACATCCGGAAAGTCCTGTGGACTT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 GCCACGTTTGTATCATCTGCTCTGTTTGTACAGAAAGTGTGTAGTGGTTTG 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 ArgLeuTyrPheIleLeuLeuLeuIlePheLeuLeuLeuIleAlaGlyIleLeu 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 310 GGATATGTTTACAGACAAAGGTGGAAATAGAGTTGATCGACATTCAG---AAAGTG 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 TATAAGACCTACATGAACCAACCTGATGCTGTAGCGGCTATTGATTATGTACAG 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 AGACAGCTGATTTGTGGAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 487 AAA-----GAAACCAAAAAACAGAGTGTCCCTTTAGCTGTGCAGAGAGCTGCCAGC 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 TTTCAGCTATTACGCTGGGCGATGCTGTGCTTTC 693
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```

RESULT 10

US-09-499-781-2
; Sequence 2, Application US/09499781
; Patent No. 6498014
; GENERAL INFORMATION:

; APPLICANT: Testa, Jacqueline E.
; APPLICANT: Quigley, James P.
; APPLICANT: Seandel, Marco
; TITLE OF INVENTION: MONOCLONAL ANTIBODIES THAT RECOGNIZE ANTIGENS
; TITLE OF INVENTION: ASSOCIATED WITH TUMOR METASTASIS
; FILE REFERENCE: SUNY
; CURRENT APPLICATION NUMBER: US/09/499,781
; CURRENT FILING DATE: 2000-02-08
; PRIOR APPLICATION NUMBER: 09/333,599
; PRIOR FILING DATE: 1999-06-15
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-499-781-2

Alignment Scores:
Pred. No.: 1.07e-28 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservatives: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 2 Gaps: 4

US-10-608-388A-1 (1-759) x US-09-499-781-2 (1-253)

```
QY 10 TGGGGCATACCTCTCCAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 70 GCTGGCATTTATGCTATGTGGAGCGCTATGCTTTCATCACTTATGATGACTATGACCAC 129
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 130 TTCTTTGAAGATGTATACCGCTCATCCCTGCTGTAGTATCATATGCTGTAGGAGCCCTG 189
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValAlaGlyThrVal 70
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 190 CTTTTCATCATGGCTAAATGGCTGTGCGCACATCCGGAAAGTCCTGTGGACTT 249
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 250 GCCACGTTTGTATCATCTGCTCTGTTTGTACAGAAAGTGTGTAGTGGTTTG 309
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 91 ArgLeuTyrPheIleLeuLeuLeuIlePheLeuLeuLeuIleAlaGlyIleLeu 110
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 310 GGATATGTTTACAGACAAAGGTGGAAATAGAGTTGATCGACATTCAG---AAAGTG 366
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 367 TATAAGACCTACATGAACCAACCTGATGCTGTAGCGGCTATTGATTATGTACAG 426
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 427 AGACAGCTGATTTGTGGAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 487 AAA-----GAAACCAAAAAACAGAGTGTCCCTTTAGCTGTGCAGAGAGCTGCCAGC 540
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValAla 190
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 541 AATTGTAATGGCAGCTGGCCCAACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyGlyCysIle 209
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 595 GCTCTAGTAGTAGAGAGCTACAGAAATCATGATGCTATGCTGTGCGGCGGCGACTGGCA 654
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
QY 655 TTTCAGCTATTACGCTGGGCGATGCTGTGCTTTC 693
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
```



```
Alignment Scores:
Pred. No.: 2,32e-28 Length: 245
Score: 329.00 Matches: 74
Percent Similarity: 50.4% Conservative: 43
Best Local Similarity: 31.9% Mismatches: 93
Query Match: 23.0% Indels: 22
DB: 2 Gaps: 5

US-10-608-388A-1 (1-759) x US-10-012-231A-4 (1-245)
QY 16 ATCACTCTCCCAAGACCGTGGTCTTTCTCAACCTCATCTTCTGGGGGGGAGCTGGC 75
Db 14 ILeThrCysPheLysSerValLeuLeuIleThrPheIlePheThrGlyVal 33
QY 76 ATTTTATGCTATGGGAGCTATGCTTTCATCATCTATGATGACTATGACCTCTTT 135
Db 34 ILeLeuLeuAlaValGlyIleThrPglyLysValSerLeuGluAsnTyrPheSerLeuLeu 53
QY 136 GAAGATGTGTACAGCTCATCCCTGCTGTAGTATCATAGCTGTAGGAGCCCTGCTTTTC 195
Db 54 AsnGluLysAlaThrAsnValPro---PheValLeuIleAlaThrGlyThrValIleIle 72
QY 196 ATCATTTGGCTAATGGCTGCTGTGCACAAATCCGGGAAAGTCGCTGTGGACTTGCACG 255
Db 73 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 92
QY 256 TTGTGTCATCTCTGCTCTTGGTTTGTACAGAGTCTTGTAGTGGTGTGGGATAT 315
Db 93 TyrAlaMetPheLeuThrLeuValPheLeuValGluLeuValAlaIleValGlyPhe 112
QY 316 GTTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAGAAAGTGTATAAGACC 375
Db 113 ValPheArgHisGluIleLysAsnSerPheLysAsnAsnTyrGluLysAlaLeuLysGln 132
QY 376 TACAATGAACCAACCTGATGCTGTAGCGGGCTATTGATTATGATGACAGACAGCTG 435
Db 133 TyrAsnSerThrGly---AspTyrArgSerHisAlaValAspLysIleGlnAsnThrLeu 151
QY 436 CATTGTGTGGAATTCACACTACTCAGATGGGAAATACAGATTGGTTCAAGAAACC 495
Db 152 HisCysGlyValThrAspTyrArgAspTrpThrAspThrAsnTyrTyrSerGlu--- 170
QY 496 AAAAAACAGAGTGCCTCTTAGCTGTGCAGA-----GAGACT 534
Db 171 -----LysGlyPheProLysSerCysLysLeuGluAspCysThrProGlnArgAsp 188
QY 535 GCCAGCAATTTGATGTCAGCGCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAG 594
Db 189 AlaAspLysValAsnAsn-----GluGlyCysPhe 198
QY 595 GCTCTAGTAGAAGAGCTACAGAATATCATGATGATGTGATCTGGGGCCGACCTGGCA 654
Db 199 IleLysValMetThrIleGluSerGluMetGlyValValAlaGlyIleSerPheGly 218
QY 655 TTTCAGCTATTTCAGCTGCTGGGAGTCTGTGTGCT 690
Db 219 ValAlaCysPheGlnLeuIleGlyIlePheLeuAla 230

RESULT 13
US-10-015-389A-4
; Sequence 4, Application US/10015389A
; Patent No. 6938436
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnovers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
```

```
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830PIC48
; CURRENT APPLICATION NUMBER: US/10/015,389A
; CURRENT FILING DATE: 2002-06-25
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 4
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-42
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: 19-42, 61-83, 92-114, 209-230
; OTHER INFORMATION: Transmembrane Domains
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 69-80, 211-222
; OTHER INFORMATION: Prokaryotic Membrane Lipoprotein Lipid Attachment Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 75-81, 78-84, 210-216, 214-220, 226-232
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 134-138
; OTHER INFORMATION: N-Glycosylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 160-168, 160-169
; OTHER INFORMATION: Tyrosine Kinase Phosphorylation Site.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: unknown amino acid
; US-10-015-389A-4
```

```
Alignment Scores:
Pred. No.: 2,32e-28 Length: 245
Score: 329.00 Matches: 74
Percent Similarity: 50.4% Conservative: 43
Best Local Similarity: 31.9% Mismatches: 93
Query Match: 23.0% Indels: 22
DB: 2 Gaps: 5
```

US-10-608-388A-1 (1-759) x US-10-015-389A-4 (1-245)

```
QY 16 ATCACTCTCCCAAGACCGTGGTCTTTCTCAACCTCATCTTCTGGGGGGGAGCTGGC 75
Db 14 ILeThrCysPheLysSerValLeuLeuIleThrPheIlePheThrGlyVal 33
QY 76 ATTTTATGCTATGGGAGCTATGCTTTCATCATCTATGATGACTATGACCTCTTT 135
Db 34 ILeLeuLeuAlaValGlyIleThrPglyLysValSerLeuGluAsnTyrPheSerLeuLeu 53
QY 136 GAAGATGTGTACAGCTCATCCCTGCTGTAGTATCATAGCTGTAGGAGCCCTGCTTTTC 195
Db 54 AsnGluLysAlaThrAsnValPro---PheValLeuIleAlaThrGlyThrValIleIle 72
QY 196 ATCATTTGGCTAATGGCTGCTGTGCACAAATCCGGGAAAGTCGCTGTGGACTTGCACG 255
Db 73 LeuLeuGlyThrPheGlyCysPheAlaThrCysArgAlaSerAlaTrpMetLeuLysLeu 92
QY 256 TTGTGTCATCTCTGCTCTTGGTTTGTACAGAGTCTTGTAGTGGTGTGGGATAT 315
```



```
Db      219 ValAlaCysPheGlnLeuIleGlyIlePheLeuAla 230
RESULT 15
US-10-015-671A-4
; Sequence 4, Application US/10015671A
; Patent No. 6946263
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan I.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gao, Wei-Qiang
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2830P1C47
; CURRENT APPLICATION NUMBER: US/10/015,671A
; CURRENT FILING DATE: 2001-12-11
; Prior application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 477
; SEQ ID NO 4
; LENGTH: 245
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: sig_peptide
; LOCATION: 1-42
; OTHER INFORMATION: Signal Peptide
; FEATURE:
; NAME/KEY: TRANSMEM
; LOCATION: 19-42, 61-83, 92-114, 209-230
; OTHER INFORMATION: Transmembrane Domains
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 69-80, 211-222
; OTHER INFORMATION: Prokaryotic Membrane Lipoprotein Lipid Attachment Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 75-81, 78-84, 210-216, 214-220, 226-232
; OTHER INFORMATION: N-Myristoylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 134-138
; OTHER INFORMATION: N-Glycosylation Site.
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 160-168, 160-169
; OTHER INFORMATION: Tyrosine Kinase Phosphorylation Site.
; FEATURE:
; NAME/KEY: unsure
; LOCATION: 233
; OTHER INFORMATION: unknown amino acid
US-10-015-671A-4
Alignment Scores:
Pred. No.:      2,32e-28      Length:      245
Score:          329.00      Matches:      74
Percent Similarity: 50.4%      Conservative: 43
Best Local Similarity: 31.9%      Mismatches:  93
Query Match:    23.0%      Indels:      22
DB:              2          Gaps:          5
```

US-10-608-388A-1 (1-759) x US-10-015-671A-4 (1-245)

QY 16 ATCACTCTCCAGACGGTCTGCTTTCTCAACCTCATCTTCTGGGGGGCAGCTGGC 75

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:48:29 ; Search time 30.6 Seconds
(without alignments)
2072.761 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atggggcagcgccgcatcac.....tcactggcggaacctatgca 759

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 3735138

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODE=frame+n2p.model -DEV=xlp
-Q=/abss/ABSSWEB.spool/US10608388/runat_04042006_150706_14321/app_query.fasta_1
-DB=Published Applications AA Main -OFMT=fastan -SUFFIX=n2p.rapbm
-MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=-1
-MATRIX=bloum62 -TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pct
-THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext
-HEAPSIZES=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10608388 @CGN 1.1 307 @runat_04042006_150706_14321 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications AA Main:

1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
6: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
1	1336	93.5	253	3	US-09-155-008-3
2	1336	93.5	253	3	US-09-983-000A-18
3	1336	93.5	253	4	US-10-223-085-66
4	1336	93.5	253	4	US-10-223-084-66
5	1336	93.5	253	4	US-10-223-088-66
6	1336	93.5	253	4	US-10-223-090-66
7	1336	93.5	253	4	US-10-223-087-66
8	1336	93.5	253	4	US-10-223-083-66
9	1336	93.5	253	4	US-10-223-089-66
10	1336	93.5	253	4	US-10-223-081-66
11	1336	93.5	253	4	US-10-223-082-66

12	1336	93.5	253	4	US-10-305-654-66	Sequence 66, Appl
13	1336	93.5	253	4	US-10-081-056-66	Sequence 66, Appl
14	1336	93.5	253	5	US-10-652-981-18	Sequence 18, Appl
15	1336	93.5	253	5	US-10-631-467-635	Sequence 635, Appl
16	1332	93.2	253	4	US-10-156-136-23	Sequence 23, Appl
17	1332	93.2	253	6	US-11-041-419-23	Sequence 23, Appl
18	1300	91.0	252	5	US-10-631-467-1431	Sequence 1431, Appl
19	1301	91.0	252	4	US-10-453-478-17	Sequence 17, Appl
20	453	31.7	222	4	US-10-037-417-81	Sequence 81, Appl
21	384	26.9	254	3	US-09-934-268-4	Sequence 4, Appl
22	384	26.9	254	4	US-10-162-435-38	Sequence 38, Appl
23	384	26.9	254	5	US-10-860-779-38	Sequence 38, Appl
24	368.5	25.8	184	3	US-09-930-512-55	Sequence 55, Appl
25	352	24.6	166	3	US-09-976-782-39	Sequence 39, Appl
26	343.5	24.0	244	4	US-10-156-136-37	Sequence 37, Appl
27	343.5	24.0	244	5	US-10-934-998-96	Sequence 96, Appl
28	343.5	24.0	244	6	US-11-041-419-37	Sequence 37, Appl
29	343.5	24.0	249	5	US-10-756-149-4994	Sequence 4994, Appl
30	334.5	23.4	244	4	US-10-205-194-105	Sequence 105, Appl
31	333.5	23.3	245	3	US-09-823-356-15	Sequence 15, Appl
32	333.5	23.3	245	3	US-09-729-674-90	Sequence 90, Appl
33	333.5	23.3	245	4	US-10-156-136-22	Sequence 22, Appl
34	333.5	23.3	245	4	US-10-024-298A-89	Sequence 89, Appl
35	333.5	23.3	245	4	US-10-042-211A-89	Sequence 89, Appl
36	333.5	23.3	245	4	US-10-617-217A-89	Sequence 89, Appl
37	333.5	23.3	245	4	US-10-024-298A-89	Sequence 89, Appl
38	333.5	23.3	245	5	US-10-913-553-90	Sequence 90, Appl
39	333.5	23.3	245	5	US-10-696-639-63	Sequence 63, Appl
40	333.5	23.3	245	6	US-11-041-419-22	Sequence 22, Appl
41	333.5	23.3	284	4	US-10-106-698-6305	Sequence 6305, Appl
42	332	23.2	253	4	US-10-153-668-476	Sequence 476, Appl
43	332	23.2	253	4	US-10-156-136-35	Sequence 35, Appl
44	332	23.2	253	6	US-11-041-419-35	Sequence 35, Appl
45	332	23.2	282	3	US-09-925-301-1234	Sequence 1234, Appl

ALIGNMENTS

RESULT 1
US-09-155-008-3
; Sequence 3, Application US/09155008
; Patent No. US20020165378A1
; GENERAL INFORMATION:
; APPLICANT: Kato, Seishi
; APPLICANT: Sekine, Shingo
; APPLICANT: Yamaguchi, Tomoko
; TITLE OF INVENTION: Human Membrane Antigen TM4 Superfamily Protein and DNA
; FILE REFERENCE: Encoding This Protein
; FILE REFERENCE: GI 6702PCT-US
; CURRENT APPLICATION NUMBER: US/09/155,008
; CURRENT FILING DATE: 1999-09-14
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 3
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-155-008-3

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 3 Gaps: 0
US-10-608-388A-1 (1-759) x US-09-155-008-3 (1-253)

QY 1 ATGGGCCAGTGGCGCATCACCTCTCCAGACCGTGGCTGCTTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyIleThrSerSerValValValPheLeuValPheLeuLeuPhe 20


```
QY 361 AAGCTGTATAGACCTACAAATGGAACCAACCTGATGCTGTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTTGTGGATTTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTTAGCTGCTGACAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGACACCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGCTGCGGCCGACCTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTyrAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGCTGTGGGCATGCTGTGCTTGCATCTGCTGTGTCAGAAAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACAGAGCTCTCATCACTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 3

```
US-10-223-085-66
; Sequence 66 Application US/10223085
; Publication No. US20030100497A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: F3235P1C10
; CURRENT APPLICATION NUMBER: US/10/223,085
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
```

```
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 393
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-085-66
```

```
Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0
```

US-10-608-388A-1 (1-759) x US-10-223-085-66 (1-253)

```
QY 1 ATGGGGCAGTGGCGCATCACCTCTCAAGACCGTGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGCCATTTTATGCTATGTGGGAGCCTATGTCTTCATCATGTATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCATTCTTTGAAGATGTATACAGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGCTAATTGGCTGTGTGCCACAATCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGCACTTGGCCACGTTTGTCTCATCTCTGCTCTTGTGTTTGTCTCAGAAAGTTGTTGA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGGTGGAAGTAAAGTGTATGTCAGACANTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAAGACCTACAAATGGAACCAACCTGATGCTGTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTTGTGGATTTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTTGTAGCTGTGCGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGACACCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGCTGCGGCCGACCTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTyrAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGCTGTGGGCATGCTGTGCTTGCATCTGCTGTGTCAGAAAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACAGAGCTCTCATCACTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 4

US-10-223-084-66

```
; Sequence 66, Application US/10223084
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C5
; CURRENT APPLICATION NUMBER: US/10/223,084
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-084-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388a-1 (1-759) x US-10-223-084-66 (1-253)

QY 1 ATGGCCGCGGCGGATGCTATGCTATGCGGAGCGGCTGCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerIysThrValLeuValPheLeuAsnLeuPhe 20
QY 61 TGGGGCGGCGGCGGATGCTATGCTATGCGGAGCGGCTATGCTTTCATCATCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysIyrValGlyAlaTyrValPheIleThrTyrAsp 40
QY 121 TATGACCACTCTTTGAAGATGTATACGCTATCCCTGCTGTAGTATGATCATCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60

181 GGAGCCCTGCTTTTCATCTATGGCTAAATGGCTGTGTGCCCAATCCGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTCCACGTTTGTTCATCATCTCTCTCTGTTTGTTCACAGAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGATATGTTTACAGAGCAAGGTGAAAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaIysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACTAATGGAACCAACCTGATCTGCTAGCCGGGCTATTGATTAT 420
Db 121 LysValTyrIysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGAGACGTCGATTTGTTGGAAATTCACACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAACCAAGAGTGTCCCTCTTAGCTGTCTCAGAGACTGCCAGC 540
Db 161 TrpPheIysGluThrIysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATGTAAATGCGACCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGATGATGATGATGATGATGATGATGATG 660
Db 201 ValValIysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTCAGCTGCTGGGCGATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgSerArg 240
QY 721 CCTGCTTACGAGCTCTCATCATCTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253

RESULT 5
US-10-223-088-66
; Sequence 66, Application US/10223088
; Publication No. US20030105012A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235P1C6
; CURRENT APPLICATION NUMBER: US/10/223,088
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
```


Db 1 MetGlyGlnCysGlyIleThrSerSerIysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGGAGCTGGCATTTTATGCTATGTGGAGGCTATGCTTCATCATCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTCTTTGAGATGCTGACACGCTCATCCCTGCTGTAGTGTATCATCATGCTGTA 180
Db 41 TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGTGCTGCTGCTGCCACAAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGACTTGGCCACGTTTGTATCATCTCTGCTCTCTGCTTTTGTTCACAGAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGTTTGGGATGTTTACAGACAAAGGTGGAAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTAAGACCTACAAATGGAACCAACCTGCTGCTGTAGTGGCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTCATGTTGTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
Qy 481 TGGTTCAGAAACCAAAACAGAGTCCCTCTTACTGCTGCTCAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGAGCTGGCCCAACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAGAATCATGATGATGATGCTGGCGCGACTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMethHisValIleTyrAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTCTGGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 7
US-10-223-087-66
; Sequence 66, Application US/10223087
; Publication No. US20030109438A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe P.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P323SP1C4
CURRENT APPLICATION NUMBER: US/10/223,087
CURRENT FILING DATE: 2002-08-16
PRIOR APPLICATION NUMBER: US 10/081,056
PRIOR FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 60/213,637
PRIOR FILING DATE: 2000-06-23
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/232,887
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30

```
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/21066
; PRIOR FILING DATE: 2001-06-29
; PRIOR APPLICATION NUMBER: PCT/US01/21735
; PRIOR FILING DATE: 2001-07-09
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-087-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-087-66 (1-253)
QY 1 ATGGGCGAGTGGGCGATCCTCTCCAGACGCTGCTGCTTCTCAACCTCATCTTC 60
DB 1 MetGlycylcysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuPhe 20
QY 61 TGGGGGCGAGTGGCATTTATGCTATGTGGGCGCTATGCTTTCATCATTTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCyserValGlyAlaIleValPheIleThrThrAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTGATGATCATGCTGA 180
DB 41 TyrAspHisPhePheGluAspValTy-ThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGCTAATGGCTGCTGCTGCTGCTGCTGCTGCTGCTG 240
DB 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTCCAGTTTGTTCATCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
DB 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGACAAAGGTGAAATGAGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyValTyValTyArgAlaValValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATGAAGCTTCAATAGAACCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTG 420
DB 121 LysValTyIleThrTyAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480
DB 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTTCAAGAAACCAAAACACAGAGTGCCTCTTAGCTGCTGCTGCTGCTGCTGCTGCTG 540
DB 161 TrpPheIleGlnThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGAATGGAGCTGGGCGCCACCTTCGACCTTATGCTGCTGCTGCTGCTGCTGCTGCTG 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
DB 201 ValValIleLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACGCTGCTGGGCGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuPhe 20

Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysA-ArgSerArgAsp 240
QY 721 CCTGCTTAGAGCTCCTCATCTCACTGCGGACCTATGCA 759
DB 241 ProAlaTyrGlnLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 8
US-10-223-083-66
; Sequence 66 Application US/10223083
; Publication No. US20030119112A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3235PIC8
; CURRENT APPLICATION NUMBER: US/10/223,083
; CURRENT FILING DATE: 2002-08-16
; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-083-66

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-223-083-66 (1-253)
QY 1 ATGGGCGAGTGGGCGATCCTCTCCAGACGCTGCTGCTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuPhe 20
```

QY 61 TGGGGGCGAGCTGCGATTTTATGCTATGTGGGAGCTATGCTTCATCACTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTATGATCATGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGCTGCCACATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGCACGTTTGTATCATCTCTGCTCTCTGTTTGTGCACAGAAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGTTTGGGATATGTTTACAGACAAAGGTGGAAATGAGTTGATCGGAGATTTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTACATGAAGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTCATTTGTTGTAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrPheGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGTGCAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGAGCTGCGCCACCCCTCCGACCTCTATGTGAGGGGTGTGAGCTCTTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGACTACAGAAATCATGATGATGATGCTGGGCGCACTGCGATTTCGA 660
Db 201 ValValLysLysLeuGlnGluIleMetHisValIleThrPalaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGCTCTGCGGATGCTGTGTGCTGTGCTATGCTGTGTGAGAGAGGATGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CTGCTTACAGAGCTCTCATCACTGCGGAACTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 9

US-10-223-089-66
; Sequence 66, Application US/10223089
; Publication No. US20030125521A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Hillan, Kenneth J.
; APPLICANT: Marsters, Scot A.
; APPLICANT: Pan, James
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Williams, P.Mickey
; APPLICANT: Ye, Weilan
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND
; TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS
; FILE REFERENCE: P3325P1C9
; CURRENT APPLICATION NUMBER: US/10/223, 089
; CURRENT FILING DATE: 2002-08-16

; PRIOR APPLICATION NUMBER: US 10/081,056
; PRIOR FILING DATE: 2002-02-20
; PRIOR APPLICATION NUMBER: US 60/213,637
; PRIOR FILING DATE: 2000-06-23
; PRIOR APPLICATION NUMBER: US 60/219,556
; PRIOR FILING DATE: 2000-07-20
; PRIOR APPLICATION NUMBER: US 60/220,624
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: US 60/220,664
; PRIOR FILING DATE: 2000-07-25
; PRIOR APPLICATION NUMBER: PCT/US00/20710
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: US 60/222,695
; PRIOR FILING DATE: 2000-08-02
; PRIOR APPLICATION NUMBER: US 09/643,657
; PRIOR FILING DATE: 2000-08-17
; PRIOR APPLICATION NUMBER: PCT/US00/23522
; PRIOR FILING DATE: 2000-08-23
; PRIOR APPLICATION NUMBER: PCT/US00/23328
; PRIOR FILING DATE: 2000-08-24
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 66
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-223-089-66
Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0
US-10-608-388a-1 (1-759) x US-10-223-089-66 (1-253)
QY 1 ATGGGCGAGCTGCGGATCATCTCCCAAGACCGTGTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGCGATTTTATGCTATGTGGGAGCTATGCTTCATCACTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTATGATCATGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGCTGCCACATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGACTTGCACGTTTGTATCATCTCTGCTCTTGTGTTTGTGCACAGAAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGTTTGGGATATGTTTACAGACAAAGGTGGAAATGAGTTGATCGGAGATTTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTACATGAAGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTCATTTGTTGTAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrPheGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGTGCAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Db 181 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAasnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGCATTATGCTATGCTGGAGCCCTATGCTTCATCACTTATGATGAC 120
Db 21 TrpGlyAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTCATCATGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGCTGTGTCACCAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTGCACGTTTGTCTATCATCTGCTCTTGGTTTGTGTCAGAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGTTTGGGATATGTTTACAGACAAAGGTGGAATGAGGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAasnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACATGGAACCAACCTGATGCTGCTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTGTTGTGAATTCACAACTACTCAGACTGCGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACACAGAGTGTCTCTTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAasnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCGCTGGCCCACTTCGACCTCTGATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAasnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATGATCATGCTGATCTGGCGCAGCTGGCATTTGCA 660
Db 201 ValValLysLeuGlnGluIleMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTGAGCTGCTGGCGATGCTGTGCTGTGATCTGCTGTGTCAGAGGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CTCGCTTACAGCTCTTCATCATCTGCGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 13

US-10-081-056-66

; Sequence 66, Application US/10081056

; Publication No. US20040043927A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Ferrara, Napoleone

; APPLICANT: Gerber, Hanspeter

; APPLICANT: Gerritsen, Mary E.

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Hillan, Kenneth J.

; APPLICANT: Marsters, Scot A.

; APPLICANT: Pan, James

; APPLICANT: Paoni, Nicholas F.

; APPLICANT: Stephan, Jean-Philippe F.

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Williams, P. Mickey

; APPLICANT: Ye, Weilan

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DIAGNOSIS AND

; TITLE OF INVENTION: TREATMENT OF DISORDERS INVOLVING ANGIOGENESIS

FILE REFERENCE: P3235PIC1
CURRENT APPLICATION NUMBER: US/10/081,056
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: PCT/US01/21735
PRIOR FILING DATE: 2001-07-09
PRIOR APPLICATION NUMBER: US 60/219,556
PRIOR FILING DATE: 2000-07-20
PRIOR APPLICATION NUMBER: US 60/220,624
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: US 60/220,664
PRIOR FILING DATE: 2000-07-25
PRIOR APPLICATION NUMBER: PCT/US00/20710
PRIOR FILING DATE: 2000-07-28
PRIOR APPLICATION NUMBER: US 60/222,695
PRIOR FILING DATE: 2000-08-02
PRIOR APPLICATION NUMBER: US 09/643,657
PRIOR FILING DATE: 2000-08-17
PRIOR APPLICATION NUMBER: PCT/US00/23522
PRIOR FILING DATE: 2000-08-23
PRIOR APPLICATION NUMBER: PCT/US00/23328
PRIOR FILING DATE: 2000-08-24
PRIOR APPLICATION NUMBER: US 60/230,978
PRIOR FILING DATE: 2000-09-07
PRIOR APPLICATION NUMBER: US 60/000,000
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 09/664,610
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 09/665,350
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US 60/242,922
PRIOR FILING DATE: 2000-10-24
PRIOR APPLICATION NUMBER: US 09/709,238
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30952
PRIOR FILING DATE: 2000-11-08
PRIOR APPLICATION NUMBER: PCT/US00/30873
PRIOR FILING DATE: 2000-11-10
PRIOR APPLICATION NUMBER: PCT/US00/32678
PRIOR FILING DATE: 2000-12-01
PRIOR APPLICATION NUMBER: US 09/747,259
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: PCT/US00/34956
PRIOR FILING DATE: 2000-12-20
PRIOR APPLICATION NUMBER: US 09/767,609
PRIOR FILING DATE: 2001-01-22
PRIOR APPLICATION NUMBER: US 09/796,498
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06520
PRIOR FILING DATE: 2001-02-28
PRIOR APPLICATION NUMBER: PCT/US01/06666
PRIOR FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: US 09/802,706
PRIOR FILING DATE: 2001-03-09
PRIOR APPLICATION NUMBER: US 09/808,689
PRIOR FILING DATE: 2001-03-14
PRIOR APPLICATION NUMBER: US 09/816,744
PRIOR FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 09/828,366
PRIOR FILING DATE: 2001-04-05
PRIOR APPLICATION NUMBER: US 09/854,208
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/854,280
PRIOR FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: US 09/866,028
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/866,034
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: PCT/US01/17092
PRIOR FILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: US 09/870,574
PRIOR FILING DATE: 2001-05-30
PRIOR APPLICATION NUMBER: PCT/US01/17443
PRIOR FILING DATE: 2001-05-30

;; PRIOR APPLICATION NUMBER: PCT/US01/17800
;; PRIOR FILING DATE: 2001-06-01
;; PRIOR APPLICATION NUMBER: PCT/US01/19692
;; PRIOR FILING DATE: 2001-06-20
;; PRIOR APPLICATION NUMBER: PCT/US01/00000
;; PRIOR FILING DATE: 2001-06-28
;; NUMBER OF SEQ ID NOS: 383
;; SEQ ID NO 66
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homosapiens
US-10-081-056-66

Alignment Scores:
Pred. No.: 3 33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservativity: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-081-056-66 (1-253)

Qy	1	ATGGCCAGTGGGCGATCACCTCCCAAGACCGTGTCTTCTTCTCAACCTCATCTTC	60
Db	1	MetGlyGlnCysGlyLeuThrSerSerValLeuValPheLeuAsnLeuPhe	20
Qy	61	TGGGGGGGAGTGGGATTTATGCTATGTTGGAGCTATGCTTCATCATCTATGATGAC	120
Db	21	TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAsp	40
Qy	121	TATGACCACTCTTTGAGATGTGTACAGCTCATCCCTGCTGTAGTGTATGATCATCTGTA	180
Db	41	TyrAspHisPheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal	60
Qy	181	GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTCCACATCCGGGAAAGTCGC	240
Db	61	GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg	80
Qy	241	TGTGACTTGGCAGCTGTTGTGCTATCTCTGCTCTTGGTTTGTTCACAGAGTTGTTGTA	300
Db	81	CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValVal	100
Qy	301	GTGTTTTGGGATGTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAG	360
Db	101	ValValLeuGlyTyrValTyrArgAlaValGluAsnGluValAspArgSerIleGln	120
Qy	361	AAAGTGTATAGACCTTACAAATGGAACCAACCTGCTGTGTAGCGGGCTATTGATTAT	420
Db	121	LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr	140
Qy	421	GTACAGACAGCTGCTGTTGTGGATTCACACTACTCAGACTGGGAAATACAGAT	480
Db	141	ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp	160
Qy	481	TGTTTCAAGAACCAAAACAGAGTGCCTCTAGCTGTGTGAGAGACTCCACAGC	540
Db	161	TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysArgGluThrAlaSer	180
Qy	541	AATTGTATGTCAGCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA	600
Db	181	AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu	200
Qy	601	GTAGTGAAGAACTACAAGAAATCATGATGCTGATCTGGGCGCGACTGGCATTTGCA	660
Db	201	ValValLysLysGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla	220
Qy	661	GCTATTCAGCTCTGGGATGCTGTGCTTCATGCTGTGTGAGAGGAGTAGAGAT	720
Db	221	AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp	240
Qy	721	CCTGCTTACGAGCTCTCATCTACTGCGGAACCTATGCA	759

Db 241 ProAlaTyrGluLeuLeuThrGlyGlyThrTyrAla 253
RESULT 14
US-10-652-981-18
;; Sequence 18, Application US/10652981
;; Publication No. US20050074400A1
;; GENERAL INFORMATION:
;; APPLICANT: AGY Therapeutics
;; APPLICANT: Melcher, Thorsten
;; APPLICANT: Mueller, Sabine
;; APPLICANT: Chin, Daniel
;; TITLE OF INVENTION: USE OF PROTEIN BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUAL
;; FILE REFERENCE: 263/180 -- Peagleman -- AGY
;; CURRENT APPLICATION NUMBER: US/10/652,981
;; CURRENT FILING DATE: 2003-08-28
;; PRIOR APPLICATION NUMBER: US/09/983,000A
;; PRIOR FILING DATE: 2001-10-17
;; NUMBER OF SEQ ID NOS: 35
;; SOFTWARE: PatentIn version 3.1
;; SEQ ID NO 18
;; LENGTH: 253
;; TYPE: PRT
;; ORGANISM: Homo sapiens
;; FEATURES:
;; NAME/KEY: DOMAIN
;; LOCATION: (1)..(11)
;; OTHER INFORMATION: Cytoplasmic (Potential)
;; FEATURE:
;; NAME/KEY: Gene
;; LOCATION: (1)..(253)
;; OTHER INFORMATION: Tetraspanin-3
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (12)..(32)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (33)..(50)
;; OTHER INFORMATION: Extracellular (Potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (51)..(71)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (72)..(85)
;; OTHER INFORMATION: Cytoplasmic (potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (86)..(106)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (107)..(212)
;; OTHER INFORMATION: Extracellular (potential)
;; FEATURE:
;; NAME/KEY: TRANSMEM
;; LOCATION: (213)..(233)
;; OTHER INFORMATION: Potential
;; FEATURE:
;; NAME/KEY: DOMAIN
;; LOCATION: (234)..(253)
;; OTHER INFORMATION: Cytoplasmic (potential)
;; FEATURE:
;; NAME/KEY: CARBOHYD
;; LOCATION: (127)..(127)
;; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
;; FEATURE:
;; NAME/KEY: CARBOHYD
;; LOCATION: (152)..(152)
;; OTHER INFORMATION: N-linked (GLCNAC...) (potential)
;; FEATURE:

NAME/KEY: CARBOHYD
LOCATION: (167)...(167)
OTHER INFORMATION: N-linked (GLCNAC...) (potential)
FEATURE:
NAME/KEY: CARBOHYD
LOCATION: (183)...(183)
OTHER INFORMATION: N-linked (GLCNAC...) (potential)
US-10-652-981-18

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-652-981-18 (1-253)

```
QY 1 ATGGGCCAGTCGGGCATCACTCTCCAAAGACGCTGCTGCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGCTGGGAGCCTATGCTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACACACTCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTGGGCTAATTTGGCTGTGCTGCACAAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysAlaThrIleArgLeuSerArg 80
QY 241 TGTGGACTTGGCAGCTTGTCTATCATCTCTGCTTGTGTTTGTACAGAAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGTTTTGGGATATGTTTACAGAACAAAGTGGAATAAGGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACAAATGGAACCACTGCTGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLeuSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCTATGTTGTGGAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAAGTGCTGCTTACAGAGAGCTGCGCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGTGCTGGCGGCACCTGCGCATTTGCA 660
DB 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaLeuAlaPheAla 220
QY 661 GCTATTGCTGGGATGCTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACAGCTCTCATCCTGCGGACCTATGCA 759
DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 15

US-10-631-467-635

Sequence 635, Application US/10631467
Publication No. US20050208496A1
GENERAL INFORMATION:
APPLICANT: Genex Research Inc.
TITLE OF INVENTION: Method for testing for bronchial asthma, or chronic obstructiv
FILE OF INVENTION: disease
FILE REFERENCE: 3462.1005-000
CURRENT APPLICATION NUMBER: US/10/631,467
CURRENT FILING DATE: 2003-07-31
PRIOR APPLICATION NUMBER: JP 2003-077212
PRIOR FILING DATE: 2003-03-20
PRIOR APPLICATION NUMBER: JP 2002-229312
PRIOR FILING DATE: 2002-08-06
NUMBER OF SEQ ID NOS: 2086
SOFTWARE: Patent in version 3.1
SEQ ID NO 635
LENGTH: 253
TYPE: PRT
ORGANISM: Homo sapiens
US-10-631-467-635

Alignment Scores:
Pred. No.: 3,33e-125 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-631-467-635 (1-253)

```
QY 1 ATGGGCCAGTCGGGCATCACTCTCCAAAGACGCTGCTGCTTTCTCAACCTCATCTTC 60
DB 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGCTGGCATTATATGCTATGCTGGGAGCCTATGCTTTCATCATTATGATGAC 120
DB 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACACACTCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTA 180
DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCATTGGGCTAATTTGGCTGTGCTGCACAAATCCGGGAAGTCGC 240
DB 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysAlaThrIleArgLeuSerArg 80
QY 241 TGTGGACTTGGCAGCTTGTCTATCATCTCTGCTTGTGTTTGTACAGAAGTTGTTGTA 300
DB 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGTTTTGGGATATGTTTACAGAACAAAGTGGAATAAGGTTGATCGCAGCATTCAG 360
DB 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAGTGTATAGACCTACAAATGGAACCACTGCTGCTGCTAGCCGGCTATTGATTAT 420
DB 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLeuSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCTATGTTGTGGAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAAGTGCTGCTTACAGAGAGCTGCGCAGC 540
DB 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTAGGGGTGTGAGGCTCTA 600
DB 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGATGTGCTGGCGGCACCTGCGCATTTGCA 660
```

Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTyrAlaAlaLeuAlaPheAla 220
QY 661 GCTATTTCAGCTGCTGGGCGATGCTGTGCTTGCATCGCTGTTGTGCGAAGGAGTAAAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCCTCATCATCGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

Search completed: April 4, 2006, 21:55:23
Job time : 159 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, **us-10-608-388a-1.n2p.rag**

Run on: April 4, 2006, 21:17:49 ; Search time 32.2 Seconds

(without alignments)
2071.357 Million cell updates/sec

Title: US-10-608-388a-1

Perfect score: 1429

Sequence: 1 atggggcagcgccgcatcac.....tcactggcggaacctatgca 759

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 4886326

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/abs/ABSSWEB.spool/US10608388/runat_04042006_150646_14026/app_query.fasta 1
-DB=A.Geneseq -QWMT=fastan -SUFFIX=n2p.rag -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388 @CGN_1_1_348 @runat_04042006_150646_14026 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=1 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

A.Geneseq_21.*
1: Genesep1980s.*
2: Genesep1990s.*
3: Genesep2000s.*
4: Genesep2001s.*
5: Genesep2002s.*
6: Genesep2003as.*
7: Genesep2003bs.*
8: Genesep2004s.*
9: Genesep2005s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1336	93.5	253	2 AAW27333	Aaw27333 Human mem
2	1336	93.5	253	2 AAW74469	Aaw74469 HP00966 p
3	1336	93.5	253	4 AAB92850	Aab92850 Human pro
4	1336	93.5	253	4 AAB92830	Aab92830 Human pro
5	1336	93.5	253	5 ABB84849	Abb84849 Human PRO
6	1336	93.5	253	5 ABB95455	Abb95455 Human ang
7	1336	93.5	253	6 AAE30341	Aae30341 Human tet
8	1336	93.5	253	7 ADD14059	Add14059 Human src
9	1336	93.5	253	7 ADD10355	Add10355 Human sec

10	1336	93.5	253	7 ADD11315	Add11315 Human sec
11	1336	93.5	253	7 ADD37108	Add37108 Human sec
12	1336	93.5	253	7 ADD45736	Add45736 Human pro
13	1336	93.5	253	8 ADE41316	Ade41316 Human sec
14	1336	93.5	253	8 ADH43499	Adh43499 Human PRO
15	1336	93.5	253	8 ADJ75383	Adj75383 Marker ge
16	1336	93.5	253	8 ADK82844	Adk82844 Human PRO
17	1336	93.5	253	8 ABM81655	Abm81655 Tumour-as
18	1336	93.5	253	8 ADP23080	Adp23080 PRO polyp
19	1336	93.5	253	8 ADP23078	Adp23078 PRO polyp
20	1332	93.2	253	2 AAW61621	Aaw61621 Clone HLT
21	1332	93.2	253	7 ABW01503	Abw01503 Human rec
22	1329	93.0	253	4 AAB92827	Aab92827 Human pro
23	1322	92.0	253	9 AEB98434	Aeb98434 Human HLT
24	1301	91.0	253	8 AD45735	Ad45735 Rat Prote
25	1301	91.0	253	8 ADJ76179	Adj76179 Marker ge
26	1300	91.0	252	3 AAY87784	Aay87784 Human TM4
27	1300	91.0	252	7 ABW02029	Abw02029 Human tra
28	1300	91.0	252	7 ADG47652	Adg47652 Human TM4
29	624	43.7	124	2 AAY12214	Aay12214 Human 5'
30	515	36.0	119	4 AAO07140	Aao07140 Human pol
31	384	26.9	254	9 ADY54293	Ady54293 Human 232
32	352	24.6	166	5 ABB78818	Abb78818 Tetraepan
33	343.5	24.0	244	7 ABW01517	Abw01517 Protein #
34	343.5	24.0	244	8 ADK60220	Adk60220 Angiogene
35	343.5	24.0	244	8 ADK60521	Adk60521 Angiogene
36	343.5	24.0	244	8 ADN05840	Adn05840 Antipsori
37	343.5	24.0	244	8 ADP73144	Adp73144 Angiogene
38	343.5	24.0	244	9 AEB98448	Aeb98448 Human TAL
39	343.5	24.0	249	8 ADO55160	Ado55160 Protein #
40	342	23.9	253	7 ADD48735	Add48735 Rat Prote
41	340	23.8	253	3 AAY69779	Aay69779 Mouse tum
42	336	23.5	253	5 AAO18875	Aao18875 Simian CD
43	334.5	23.4	244	7 ADS85224	Ads85224 Mouse cel
44	333.5	23.3	245	2 AAW61620	Aaw61620 Clone HSB
45	333.5	23.3	245	2 AAY28677	Aay28677 Human bxl

ALIGNMENTS

RESULT 1
AAW27333
ID AAW27333 standard; protein; 253 AA.

XX AAW27333;
XX AC
XX AAW27333;
XX DT 16-JAN-1998 (first entry)
XX DE
XX DE Human membrane antigen TM4 superfamily protein.

XX KW Human membrane antigen; TM4 superfamily protein; antibody; osteosarcoma;
XX KW immunomodulation; diagnosis; cancer; chemotactic; haemotopoiesis;
XX KW anti-inflammation; genetic fingerprinting; human CB63; antimicrobial;
XX KW analgesic; fertility.

XX OS Homo sapiens.

XX PN WO9733993-Al.

XX PD 18-SEP-1997.

XX PF 14-MAR-1997; 97WO-JF000811.

XX PR 15-MAR-1996; 96JP-00059571.

XX PA (SAGA) SAGAMI CHEM RES CENTRE.

XX PI Kato S, Sekine S, Yamaguchi T;

XX XX WPI; 1997-470873/43.

XX DR N-PSDB; AAT84982.

XX PT Human membrane antigen of TM4 superfamily - useful to diagnose or treat


```
QY 1 ATGGGCGAGTGGCGCATCACCTCTCTCAAGACCGTGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuIlePhe 20
QY 61 TGGGGGCGAGTGGCGCATCTTTATGCTATGTGGAGCCCTATGCTTTCATCACTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTy=ValGlyAlaTy=ValPheIleThrTy=AspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTCTGTAGTGCATGATGATGTA 180
Db 41 TyrAspHisPhePheGluAspValTy=ThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCTGGCTAATGTGGCTGTGTGCACAAATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTCCACGTTGTGCATCATCTCTCTGTTTGTTCACAGAAGTTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGATATGTTTACAGAGCAAGGTGGAAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTy=ValTy=ArgAlaLysValGluAenGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAAGACCTTACAATGGAACCAACCTGATGCTGTAGCCGGGCTATTGATTAT 420
Db 121 LysValTy=ThrTy=AsnGlyThrAsnProAspAlaLaserArgAlaIleAspTy= 140
QY 421 GTACAGAGACGTGCTATTTGTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTy=SerAspTrpGluAenThrAsp 160
QY 481 TGTTCAAAGAACCAACCAACAGAGTGTCTCTTCTAGCTGTGCAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGACCTGGCCGCCACCTTCGACCTCTATCTCAGGGGTCTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTy=AlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATCATCTGTGATCTGGCCCGCAGCTGGCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaLeuAlaPheAla 220
QY 661 GCTATTACGCTGTGGGATGCTGTGTCTGTGATGCTGTGTGTCAGAGAGCTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCTCTCATCACTGGCGGAACCTATGCA 759
Db 241 ProAlaTy=ThrLeuLeuIleThrGlyGlyThrTy=Ala 253
```

RESULT 3

AAB92850

ID AAB92850 standard; protein; 253 AA.

XX AC AAB92850;

XX DB 26-JUN-2001 (first entry)

XX DE Human protein sequence SEQ ID NO:11412.

XX KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.

XX OS Homo sapiens.

XX PN EP1074617-A2.

XX PD 07-FEB-2001.

XX PF 28-JUL-2000; 2000EP-00116126.

```
PR 29-JUL-1999; 99JP-00248036.
PR 27-AUG-1999; 99JP-00300253.
PR 11-JAN-2000; 2000JP-00118776.
PR 02-MAY-2000; 2000JP-00183767.
PR 09-JUN-2000; 2000JP-00241899.
XX (HELI-) HELIX RES INST.
XX Ota T, Isogai T, Nishikawa T, Hayaishi K, Saito K, Yamamoto J;
PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
XX WPI; 2001-318749/34.
XX
PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-
PT length cDNAs defined in the specification, and for the detection and/or
PT diagnosis of the abnormality of the proteins encoded by the full-length
PT cDNAs.
XX
PS Claim 8; SEQ ID NO 11412; 2537pp + Sequence Listing; English.
XX
CC The present invention describes primer sets for synthesising 5602 full-
CC length cDNAs defined in the specification. Where a primer set comprises:
CC (a) an oligo-dr primer and an oligonucleotide complementary to the
CC complementary strand of a polynucleotide which comprises one of the 5602
CC nucleotide sequences defined in the specification, where the
CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
CC of an oligonucleotide comprising a sequence complementary to the
CC complementary strand of a polynucleotide which comprises a 5'-end
CC sequence and an oligonucleotide comprising a sequence complementary to a
CC polynucleotide which comprises a 3'-end sequence, where the
CC oligonucleotide comprises at least 15 nucleotides and the combination of
CC the 5'-end sequence/3'-end sequence is selected from those defined in the
CC specification. The primer sets can be used in antisense therapy and in
CC gene therapy. The primers are useful for synthesising polynucleotides,
CC particularly full-length cDNAs. The primers are also useful for the
CC detection and/or diagnosis of the abnormality of the proteins encoded by
CC the full-length cDNAs. The primers allow obtaining of the full-length
CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
CC oligonucleotides, all of which are used in the exemplification of the
CC present invention
XX
SQ Sequence 253 AA;
```

Alignment Scores:

Pred. No.: 1,32e-138 Length: 253

Score: 1336.00 Matches: 253

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 93.5% Indels: 0

DB: 4 Gaps: 0

US-10-608-388A-1 (1-759) x AAB92850 (1-253)

```
QY 1 ATGGGCGAGTGGCGCATCACCTCTCTCAAGACCGTGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuIlePhe 20
QY 61 TGGGGGCGAGTGGCGCATCTTTATGCTATGTGGAGCCCTATGCTTTCATCACTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTy=ValGlyAlaTy=ValPheIleThrTy=AspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCTCTGTAGTGCATGATGATGTA 180
Db 41 TyrAspHisPhePheGluAspValTy=ThrLeuIleProAlaValIleIleAlaVal 60
QY 181 GGAGCCCTGCTTTTCATCTGGCTAATGTGGCTGTGTGCACAAATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTGGCACCGTTTGTGCATCATCTCTGTTTGTTCACAGAAGTTGTGTA 300
```

Db 81 CysGlyLeuAlaThrPheValIleLeuLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGATATGTTTACAGACAAAGGTGAAAATGAGTTGATCCGACGATTTCAG 360
 Db 101 ValValLeuGlyTyValTyArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATGGAACCAACCTGATGCTGTACCGGGCTATTGATTAT 420
 Db 121 LysValTyLysThrTyAsnGlyThrAsnProAspAlaSerArgAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTySerAspTyrGluAsnThrAsp 160
 Qy 481 TGGTTCAAGAAACCAAAACACAGAGTCCCTCTTACGCTGCTCAGAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysAspArgGluThrAlaSer 180
 Qy 541 AATTGTAATGCGACCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyAlaGluGlyCysGluAlaLeu 200
 Qy 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATCTGTGGCCGCACTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTyrAlaLeuAlaPheAla 220
 Qy 661 GCTATTAGCTGCTGGGATCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
 Qy 721 CCTGCTTACGAGCTCTCATCACTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyGluLeuLeuIleThrGlyGlyThrTyAla 253

RESULT 4

AAB92830
 ID AAB92830 standard; protein; 253 AA.
 XX
 AC AAB92830;
 XX
 DT 26-JUN-2001 (first entry)
 XX
 DE Human protein sequence SEQ ID NO:11371.
 XX
 KW Human; primer; detection; diagnosis; antisense therapy; gene therapy.
 XX
 OS Homo sapiens.
 XX
 PN EPI074617-A2.
 XX
 PD 07-FEB-2001.
 XX
 PF 28-JUL-2000; 2000EP-00116126.
 XX
 PR 29-JUL-1999; 99JP-00248036.
 PR 27-AUG-1999; 99JP-00300253.
 PR 11-JAN-2000; 2000JP-00118776.
 PR 02-MAY-2000; 2000JP-00183767.
 PR 09-JUN-2000; 2000JP-00241899.
 XX
 PA (HELI-) HELIX RES INST.
 XX
 FI Ota T, Isogai T, Nishikawa T, Hayashi K, Saito K, Yamamoto J;
 PI Ishii S, Sugiyama T, Wakamatsu A, Nagai K, Otsuki T;
 XX
 DR WPI; 2001-318749/34.
 XX
 PT Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs.
 XX
 PS Claim 8; SEQ ID NO 11371; 2537pp + Sequence Listing; English.

XX The present invention describes primer sets for synthesizing 5602 full-length cDNAs defined in the specification. Where a primer set comprises:
 CC (a) an oligo-dT primer and an oligonucleotide complementary to the
 CC complementary strand of a polynucleotide which comprises one of the 5602
 CC nucleotide sequences defined in the specification, where the
 CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination
 CC of an oligonucleotide comprising a sequence complementary to the
 CC complementary strand of a polynucleotide which comprises a 5'-end
 CC sequence and an oligonucleotide comprising a sequence complementary to a
 CC polynucleotide which comprises a 3'-end sequence, where the
 CC oligonucleotide comprises at least 15 nucleotides and the combination of
 CC the 5'-end sequence/3'-end sequence is selected from those defined in the
 CC specification. The primer sets can be used in antisense therapy and in
 CC gene therapy. The primers are useful for synthesizing polynucleotides,
 CC particularly full-length cDNAs. The primers are also useful for the
 CC detection and/or diagnosis of the abnormality of the proteins encoded by
 CC the full-length cDNAs. The primers allow obtaining of the full-length
 CC cDNAs easily without any specialised methods. AAH03166 to AAH13628 and
 CC AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893
 CC represent human amino acid sequences; and AAH13629 to AAH13632 represent
 CC oligonucleotides, all of which are used in the exemplification of the
 CC present invention
 XX
 SQ Sequence 253 AA;

Alignment Scores:
 Pred. No.: 1,32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 99.5% Indels: 0
 DB: Gaps: 0

US-10-608-388A-1 (1-759) X AAB92830 (1-253)

Qy 1 ATGGGGCAGTGGCGCATCACCTCTCCAGACCGTGTGCTCTTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 Qy 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCTATGCTTCATCACCATTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyValGlyAlaTyValPheIleThrTyAspAsp 40
 Qy 121 TATGACCACCTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATGCTGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyThrLeuIleProAlaValIleAlaVal 60
 Qy 181 GGAGCCCTGTTTTCATCATTTGGGCTAAATTTGGTGTGCTGTGCCACAATCCGGGAAAGTCG 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 Qy 241 TGTGGACTTGGCAGCTTTGTGCATCATCTCTGTTGTTTGTTCACAGAGATTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleLeuLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGGATATGTTTACAGACGAAAGGTGGAAATGAGTTGATCGCAGCATTCAG 360
 Db 101 ValValLeuGlyTyValTyArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATGGAACCAACCTGATGCTGTACCGGGCTATTGATTAT 420
 Db 121 LysValTyLysThrTyAsnGlyThrAsnProAspAlaSerArgAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTySerAspTyrGluAsnThrAsp 160
 Qy 481 TGGTTCAAGAAACCAAAACACAGAGTCCCTCTTACGCTGCTCAGAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysAspArgGluThrAlaSer 180
 Qy 541 AATTGTAATGCGACCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600

181 AsnCysAenGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 601 GTACTGAAGAGCTACAGAAATCATGATCATGCTGGCGCGCACTGGCATTTGCA 660
 201 ValVallyslsLeuGlnGluileMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 661 GCTATTACAGCTGCTGGCAGCTGCTGTGTCTTGGCATCTGTGTGTCAGAGAGTAGAGAT 720
 221 AlaileGlnLeuLeuGlyMetLeuCysAlaCysileValleuCysAraGArSerArgAsp 240
 721 CTTGCTTACGAGCTCTCATCATCTGGCGGGAACCTATGCA 759
 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253

RESULT 5

ABB84849
 ID ABB84849 standard; protein; 253 AA.

XX AC ABB84849;

XX DT 16-MAY-2002 (first entry)

XX DE Human PRO730 protein sequence SEQ ID NO:66.

XX KW Human; angiogenesis; cardiant; cytostatic; antiangiogenic; hypotensive;
 XX KW vulnery; antiarteriosclerotic; PRO agonist; trauma;
 XX KW gene therapy; cardiovascular disorder; endothelial disorder; cancer;
 XX KW angiogenic disorder; cardiac hypertrophy; atherosclerosis; hypertension;
 XX KW age-related macular degeneration; arterial restenosis; angina;
 XX KW rheumatoid arthritis; myocardial infarction; thrombophlebitis;
 XX KW lymphangitis; tumour angiogenesis; breast carcinoma; liver carcinoma;
 XX KW wound healing; chromosome mapping; gene mapping.

XX OS Homo sapiens.

XX PN WO20020690-A2.

XX PD 03-JAN-2002.

XX PF 20-JUN-2001; 2001WO-US019692.

XX PR 23-JUN-2000; 2000US-0213637P.

XX PR 20-JUL-2000; 2000US-0219556P.

XX PR 25-JUL-2000; 2000US-0220624P.

XX PR 25-JUL-2000; 2000US-0220664P.

XX PR 28-JUL-2000; 2000WO-US020710.

XX PR 02-AUG-2000; 2000US-0222695P.

XX PR 17-AUG-2000; 2000US-00643657.

XX PR 23-AUG-2000; 2000WO-US023522.

XX PR 24-AUG-2000; 2000WO-US023328.

XX PR 07-SEP-2000; 2000US-0230978P.

XX PR 18-SEP-2000; 2000US-00664610.

XX PR 18-SEP-2000; 2000US-00665350.

XX PR 24-OCT-2000; 2000US-0242922P.

XX PR 08-NOV-2000; 2000US-00709238.

XX PR 08-NOV-2000; 2000WO-US030952.

XX PR 10-NOV-2000; 2000WO-US030873.

XX PR 01-DEC-2000; 2000WO-US032678.

XX PR 20-DEC-2000; 2000US-00747259.

XX PR 20-DEC-2000; 2000WO-US034956.

XX PR 22-JAN-2001; 2001US-00767609.

XX PR 28-FEB-2001; 2001US-00796498.

XX PR 28-FEB-2001; 2001WO-US006520.

XX PR 01-MAR-2001; 2001WO-US006666.

XX PR 09-MAR-2001; 2001US-00802706.

XX PR 14-MAR-2001; 2001US-00808689.

XX PR 22-MAR-2001; 2001US-00816744.

XX PR 05-APR-2001; 2001US-00828366.

XX PR 10-MAY-2001; 2001US-00854208.

XX PR 10-MAY-2001; 2001US-00854280.

XX PR 25-MAY-2001; 2001US-00866028.

XX PR 25-MAY-2001; 2001US-00866034.

PR

PR 25-MAY-2001; 2001WO-US017092.

PR 30-MAY-2001; 2001US-00870574.

PR 30-MAY-2001; 2001WO-US017443.

PR 01-JUN-2001; 2001WO-US017800.

XX

XX (GETH) GENENTECH INC.

XX

XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;

XX Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX

XX WPI; 2002-090516/12.

DR

DR N-PSDB; ABL88104.

XX

XX One hundred and eighty seven nucleic acids encoding PRO polypeptides,

XX useful in diagnosis and treatment of cardiovascular (e.g. myocardial

XX infarction), endothelial or angiogenic disorders in a mammal.

PS

PS Claim 11; Fig 66; 565pp; English.

XX

CC ABL88072 to ABL88258 encode the PRO proteins given in ABB84817 to
 CC ABB85003. The PRO proteins and polynucleotides have cardiant, cytostatic,
 CC antiangiogenic, hypotensive, vulnery and antiarteriosclerotic
 CC activities, and can be used in gene therapy. The PRO polynucleotides,
 CC proteins, agonists and antagonists are useful for treating or diagnosing
 CC a cardiovascular, endothelial or angiogenic disorder in a mammal, e.g.
 CC cardiac hypertrophy, trauma, cancer, age-related macular degeneration,
 CC atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
 CC angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
 CC angiogenesis (such as breast carcinoma and liver carcinoma) and wound
 CC healing. The PRO polynucleotides have applications in molecular biology,
 CC including use as hybridisation probes, and in chromosome and gene
 CC mapping. ABL88259 to ABL88267 represent primers and probes used in the
 CC exemplification of the present invention

XX

SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1-32e-138 Length: 253

Score: 1336.00 Matches: 253

Percent Similarity: 100.0% Conservative: 0

Best Local Similarity: 100.0% Mismatches: 0

Query Match: 93.5% Indels: 0

DB: 5 Gaps: 0

US-10-608-388A-1 (1-759) x ABB84849 (1-253)

QY 1 ATGGGCGCAGTCGGGCATCACCTCTTCAAGACCGTCTGCTTTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAenLeuIlePhe 20

QY 61 TGGGGGGGCGAGCTGGCATTTTATGCTATGTTGGGAGCGCTATGCTTCTCATCTTATGATGAC 120

Db 21 TrpGlyAlaAlaGlyIleLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40

QY 121 TATGACCACTCTTTGAAGATGTACACGCTCATCCCTGCTGTAGTGTATCATGCTGTA 180

Db 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValValIleIleAlaVal 60

QY 181 GGAGCCCTGCTTTTTCATCATTTGGGCTAAATTGGCTGTGTGCCCAATCCGGGAAGTCGC 240

Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80

QY 241 TGTGGACTTGGCCAGCTTTGTGTGTCATCATCTGCTCTTGGTGTTCACAGAGTTGTGTGA 300

Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

QY 301 GTGGTTTTGGGATATGTTTACAGAGCAAGAGTGGAAATGAGTTTGTATCGCACATTTCAG 360

Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluasnGluValaspArgSerIleGln 120

QY 361 AAAGTGATTAAGACCTACAATGGAACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420

Db

```

Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGCAGCCTGGCCACCTTCGACCTCTATGCTAGGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATG 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTGCTGGGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCCTCATCATCTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 6
ABB95455
ID ABB95455 standard; protein; 253 AA.
AC ABB95455;
XX
DT 19-JUL-2002 (first entry)
XX
DE Human angiogenesis related protein PRO730 SEQ ID NO: 66.
XX
KW Human; angiogenesis; PRO protein; cardiovascularisation; wound; cancer;
KW atherosclerosis; cardiac hypertrophy; gene therapy; endothelial disorder;
KW cardiant; cytosclerotic; antiangiogenic; hypotensive; vulnerary;
KW antiarteriosclerotic.
XX
OS Homo sapiens.
XX
PN WO200208284-A2.
XX
PD 31-JAN-2002.
XX
PF 09-JUL-2001; 2001WO-US021735.
XX
PR 20-JUL-2000; 2000US-0219556P.
PR 25-JUL-2000; 2000US-0220624P.
PR 25-JUL-2000; 2000US-0220664P.
PR 28-JUL-2000; 2000WO-US020710.
PR 02-AUG-2000; 2000US-0222695P.
PR 17-AUG-2000; 2000US-00643657.
PR 23-AUG-2000; 2000WO-US023522.
PR 24-AUG-2000; 2000WO-US023328.
PR 07-SEP-2000; 2000US-0230978P.
PR 18-SEP-2000; 2000US-00664610.
PR 18-SEP-2000; 2000US-00665350.
PR 24-OCT-2000; 2000US-0242922P.
PR 08-NOV-2000; 2000US-00709238.
PR 08-NOV-2000; 2000WO-US030952.
PR 10-NOV-2000; 2000WO-US030873.
PR 01-DEC-2000; 2000WO-US032678.
PR 20-DEC-2000; 2000US-00747259.
PR 20-DEC-2000; 2000WO-US034956.
PR 22-JAN-2001; 2001US-00767609.
PR 28-FEB-2001; 2001US-00796498.
PR 28-FEB-2001; 2001WO-US006520.
PR 01-MAR-2001; 2001WO-US006666.
PR 09-MAR-2001; 2001US-00802706.
PR 14-MAR-2001; 2001US-00808689.

```

```

PR 22-MAR-2001; 2001US-00816744.
PR 05-APR-2001; 2001US-00828366.
PR 10-MAY-2001; 2001US-00854208.
PR 10-MAY-2001; 2001US-00854280.
PR 25-MAY-2001; 2001US-00866028.
PR 25-MAY-2001; 2001US-00866034.
PR 25-MAY-2001; 2001WO-US017092.
PR 30-MAY-2001; 2001US-00870574.
PR 30-MAY-2001; 2001WO-US017443.
PR 01-JUN-2001; 2001WO-US017800.
PR 20-JUN-2001; 2001WO-US019692.
XX
( GETH ) GENENTECH INC.
PA (BAKE/) BAKER K P.
PA (FERE/) FERRARA N.
PA (GERE/) GERBER H.
PA (GERR/) GERRITSEN M E.
PA (GODD/) GODDARD A.
PA (GODO/) GODOWSKI P J..
PA (GURN/) GURNEY A L.
PA (HILL/) HILLAN K J.
PA (MARS/) MARSTERS S A.
PA (PANJ/) PAN J.
PA (PAON/) PAONI N F.
PA (STEP/) STEPHAN J P.
PA (WATA/) WATANABE C K.
PA (WILL/) WILLIAMS P M.
PA (WOOD/) WOOD W I.
XX
Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;
WFI; 2002-171999/22.
DR N-PSDB; ABL95593.
XX
One hundred and eighty seven nucleic acids encoding PRO polypeptides,
useful in diagnosis and treatment of cardiovascular (e.g. myocardial
infarction), endothelial or angiogenic disorders in a mammal.
XX
Claim 11; Fig 66; 567pp; English.
XX
The present invention provides the protein and coding sequences of human
PRO proteins. These are useful for treating or diagnosing a
cardiovascular, endothelial or angiogenic disorder, including cardiac
hypertrophy, trauma, cancer, age-related macular degeneration,
atherosclerosis, hypertension, arterial restenosis, rheumatoid arthritis,
angina, myocardial infarctions, thrombophlebitis, lymphangitis, tumour
angiogenesis (such as breast carcinoma and liver carcinoma) and wound
healing. The present sequence is a PRO protein of the invention
XX
SQ Sequence 253 AA;
Alignment Scores:
Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 5 Gaps: 0
US-10-608-388A-1 (1-759) x ABB95455 (1-253)
Qy 1 ATGGCCAGTCGGGCATCAGCTCTCCAGACCGCTGCTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGCAGCTGGCATTATTTATGCTATGTGGAGCCTATGCTTCATCATCTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACCTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATGCTCTTA 180

```



```
Db 41 TyraephHisPhePheGluAaspValTyThrLeuileProAlaValValIleileAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATGGCTAATGGCTGCTGCCACATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuileGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTCCACAGTGTGTGCATCATCTCTCTTGGTTTGTGCAGAGAAGTTGTGTGA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGGTTTGGGATGATGTTTACAGACCAAGGTGGAATACAGTTGATCCACAGATTGAG 360
Db 101 ValValLeuGlyTyThrValTyArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAGACCTACATGAAACCAACCCCTGATGCTGCTAGCCGGCTATTGATTAT 420
Db 121 LysValTyThrTyArgGlyThrAsnProAspAlaLysSerArgAlaIleAspTyThr 140
Qy 421 GTACAGACAGCTGCTGCTTGTGTGAATTCACAACCTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyThrSerAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACCAAGAGTGTCCCTCTTACCTGCTGCTGAGAGAGCTGCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCAGCTCTATGCTGAGGGTGTGGGCTCTTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAGAAATCATGATCATGCTGCTGCTGCTGCTGCTGCTGCTGCTG 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTGAGCTGTGGGCAATGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CCTGCTTACAGCTCTCTCATCTACCTGCGGCACTTATGCA 759
Db 241 ProAlaTyGluLeuLeuIleThrGlyTyThrTyAla 253

RESULT 7
AAE30341
ID AAE30341 standard; protein; 253 AA.
AC AAE30341;
XX
XX
XX 24-FEB-2003 (first entry)
XX Human tetraspan 3 protein.
XX Brain; tumour protein target; Tbt; ischaemic stroke; cancer; epilepsy;
XX schizophrenia; depression; Alzheimer's disease; Parkinson's disease;
XX Huntington's chorea; traumatic head injury; dementia; stupor; headache;
XX coma; vertigo; weakness; myasthenia gravis; cerebrovascular disorder;
XX infection; multiple sclerosis; pregnancy; medical illness; vasotropic;
XX metabolic deficiency; cerebroprotective; antidepressant; antibacterial;
XX cytostatic; nootropic; analgesic; fungicide; virucide; tetraspan 3;
XX human.
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX Domain 1..11 /note= "Cytoplasmic domain"
XX Domain 12..32 /note= "Transmembrane domain"
XX Domain 33..50 /note= "Extracellular domain"
XX Domain 51..71 /note= "Transmembrane domain"
XX Domain 72..85
```

```
FT Domain /note= "Cytoplasmic domain"
FT 85..106 /note= "Transmembrane domain"
FT 107..212 /note= "Extracellular domain"
FT 213..233 /note= "Transmembrane domain"
FT 234..235 /note= "Cytoplasmic domain"
XX
```

W0200276510-A1.

03-OCT-2002.

22-MAR-2002; 2002WO-US008992.

23-MAR-2001; 2001US-00816703.

17-OCT-2001; 2001US-00983000.

(AGYT-) AGY THERAPEUTICS INC.

Mueller S, Melcher T, Chin DJ;

WPI; 2003-029903/02.

N-PSDB; AAD48134.

Developing active agents that modulate the activity of a brain tumor protein target gene or gene product for treating e.g. stroke or cancer, comprises contacting an agent with a brain tumor protein.

Claim 1; Page 125-127; 135pp; English.

The invention relates to a method for developing biologically active agents that modulate activity of a brain tumour protein target (Tbt) gene or gene product. The method is useful for developing biologically active agents that modulate the activity of a brain tumour protein target gene or gene product. Compounds that bind to the brain tumour proteins are useful for treating e.g. ischaemic stroke, brain cancer, epilepsy, schizophrenia, depression, Alzheimer's disease, Parkinson's disease, Huntington's chorea, traumatic head injury, dementia, stupor, headache, coma, vertigo, weakness, myasthenia gravis, cerebrovascular disorders, infectious disorders (including fungal, bacterial, viral and parasitic infections), multiple sclerosis, and other complications associated with pregnancy, medical illness, alcohol and substance abuse, toxins and metabolic deficiencies. The brain tumour proteins may also be used to raise antibodies. The present sequence is human tetraspan 3 protein used to illustrate the method of the invention

SQ Sequence 253 AA;

Alignment Scores:

Pred. No.:	1.32e-138	Length:	253
Score:	1336.00	Matches:	253
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	93.5%	Indels:	0
DB:	6	Gaps:	0

US-10-608-388A-1 (1-759) x AAE30341 (1-253)

```
Qy 1 ATGGGCCAGTGGCGCATCACCTCTCCAGAGCCGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGGCAGCTGGCATTATGCTTATGTGGGAGCCTATGCTTTCATCATCTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyValGlyAlaTyValPheIleThrTyArgAsp 40
Qy 121 TATGACCACTTTTGAAGATGTGTACAGCTCATCTCCCTGCTGTAGTGTAGTGTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyThrLeuIleProAlaValIleIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGGTAAATTGGCTGCTGCGCACAAATCGGGAAGTCGC 240
```

Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 Qy 241 TGTGGACTTGCACGTTTGTGTCATCTCTGCTCTGTTTGTTCACAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGATATGTTACAGACCAAGGTGGAATGAGTTGATCCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATAGGAACCAACCTGATGCTAGCCGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
 Qy 481 TGGTTCAAGAAACCAAAACCAAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 Qy 541 AATTGTAAATGCGACCTGGCCACCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 Qy 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleThrAlaAlaLeuAlaPheAla 220
 Qy 661 GCTATTGAGCTGGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
 Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 8

ADD14059
 ID ADD14059 standard; protein; 253 AA.
 XX
 AC ADD14059;
 XX
 DT 01-JAN-2004 (first entry)
 XX
 DE Human src biomarker polypeptide SEQ ID NO:248.
 XX
 KW predictor set; protein tyrosine kinase activity modulator;
 KW protein tyrosine kinase pathway; protein tyrosine kinase; cyrostatic;
 KW gene therapy; drug sensitivity; genetic profile; cancer; human.
 XX
 OS Homo. sapiens.
 XX
 PN WO2003062395-A2.
 XX
 PD 31-JUL-2003.
 XX
 PF 17-JAN-2003; 2003WO-US001981.
 XX
 PR 18-JAN-2002; 2002US-0350061P.
 XX
 PA (BRIM) BRISTOL-MYERS SQUIBB CO.
 XX
 PI Huang F, Fairchild CR, Lee FY, Shaw P;
 XX
 DR WPI; 2003-636735/60.
 DR N-PSDB; ADD14654.
 XX
 PT New polynucleotides and polypeptides for predicting the activity of
 PT compounds that interact with protein tyrosine kinases and/or protein
 PT tyrosine kinase pathways.

XX Claim 10; SEQ ID NO 248; 139pp; English.

XX The present invention describes a predictor set comprising a plurality of
 CC polynucleotides or polypeptides whose expression pattern is predictive of
 CC the response of cells to treatment with a compound that modulates protein
 CC tyrosine kinase activity or members of the protein tyrosine kinase
 CC pathway. Also described: (1) predicting whether a compound is capable of
 CC modulating the activity of cells, comprising obtaining a sample of cells,
 CC determining whether the cells express a plurality of markers, and
 CC correlating the expression of the markers to the compound's ability to
 CC modulate the activity of the cells; (2) a plurality of cell lines for
 CC identifying polynucleotides and polypeptides whose expression levels
 CC correlate with compound sensitivity or resistance of cells associated
 CC with a disease state; and (3) identifying polynucleotides and
 CC polypeptides that predict compound sensitivity or resistance of cells
 CC associated with a disease state, comprising subjecting the plurality of
 CC cell lines to one or more compounds, analysing the expression pattern of
 CC a microarray of polynucleotides or polypeptides, and selecting
 CC polynucleotides or polypeptides that predict the sensitivity or
 CC resistance of cells associated with a disease state by using the
 CC expression pattern of the microarray. The polynucleotides and
 CC polypeptides have cyrostatic activities, and can be used in gene therapy.
 CC The polynucleotides and polypeptides are useful in predicting the
 CC activity of compounds that interact with protein tyrosine kinases and/or
 CC protein tyrosine kinase pathways. These may be used in determining drug
 CC sensitivity in patients to allow the development of individualized
 CC generic profiles which aid in treating diseases and disorders (e.g.
 CC cancer) based on patient response at a molecular level. The present
 CC sequence is used in the exemplification of the present invention.

XX Sequence 253 AA;

Alignment Scores:

Pred. No.: 1,32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: Gaps: 0

US-10-608-388A-1 (1-759) x ADD14059 (1-253)

Qy 1 ATGGGCGCAGTGGCGCATCACCTCTCCAGACCGTGTGCTTCTTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 Qy 61 TGGGGGCGAGCTGGCATTTTATGCTATGTGGAGCCTATGCTTTCATCATCTTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 Qy 121 TATGACCACTCTTTGAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleIleAlaVal 60
 Qy 181 GGAGCCCTGCTTTTTCATCATTTGGCTAATTTGGCTGTGTCGCCCAATCCGGGAAAGTCGC 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 Qy 241 TGTGGACTTGCACGTTTGTGTCATCTCTCTCTGTTTGTGTTTGTGTCAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
 Qy 301 GTGGTTTGGATATGTTTACAGACCAAGGTGGAATGAGTTGATCCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 Qy 361 AAAGTGATTAAGACTCAATAGGAACCAACCTGATGCTAGCCGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaIleAspTyr 140
 Qy 421 GTACAGACAGCTGCATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480

Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 QY 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATTGTAAATGACAGCTGGCCACCTTCCGACTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTACTGAAGAGCTACAGAAATCATGATCATGCTGCTGGCGGCACTGGCAATTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTGAGCTGCTGGGCGATGCTGTGCTTGTGATCGTGTGTCAGAAGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
 QY 721 CTGTCTTACGAGCTCTCATCACTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 9

ADD10355
 ID ADD10355 standard; protein; 253 AA.

XX AC ADD10355;
 XX DT 01-JAN-2004 (first entry)
 XX DE Human secreted/transmembrane PRO polypeptide #33.
 XX KW human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX OS Homo sapiens.
 XX PN US2003105011-A1.
 XX PD 05-JUN-2003.
 XX PF 16-AUG-2002; 2002US-00223084.
 XX PR 15-SEP-2000; 2000US-0232887P.
 XX PR 20-JUN-2001; 2001WO-US019692.
 XX PR 09-JUL-2001; 2001WO-US021735.
 XX PR 20-FEB-2002; 2002US-00081056.
 XX PA (GETH) GENENTECH INC.
 XX PI Baker KP, Ferrara N, Gerber H, Gerttsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX N-PSDB; ADD10354.
 XX DR WPI; 2003-810831/76.
 XX DR N-PSDB; ADD10354.
 XX PT New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX PS Claim 11; SEQ ID NO 66; 493pp; English.
 XX CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of

CC an elevated level of PGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302, or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.

XX SQ Sequence 253 AA;

Alignment Scores:
 Pred. No.: 1,32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 7 Gaps: 0

US-10-608-388A-1 (1-759) x ADD10355 (1-253)

QY 1 ATGGGGCAGTGGCGCATCACTCTCCAGACCGTGTGTCTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 QY 61 TGGGGGGCAGTGGCGCATTTTATGCTATGTGGGAGCTATGCTTCTCATCTTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrThrAsp 40
 QY 121 TATGACCACCTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
 QY 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATGGCTGTGTGCCACATCCGGGAAAGTCGC 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 QY 241 TGTGGACTTGGCCACGTTTGTTCATCTCTGCTCTCTGTTTTCACAGAGTGTGTTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluAlaVal 100
 QY 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGTGGAAAATCAGCTTGATCGCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 QY 361 AAAGTGTAAGACCTACAAATGGAACCAACCTGTAGTGTCTGAGCGGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
 QY 421 GTACAGAGACAGCTGCATTGTTGGAATTCACACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 QY 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATTGTAAATGACAGCTGGCCACCTTCCGACTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAGCTACAGAAATCATGATCATGCTGCTGGCGGCACTGGCAATTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTGAGCTGCTGGGCGATGCTGTGCTTGTGATCGTGTGTCAGAAGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
 QY 721 CTGTCTTACGAGCTCTCATCACTGGCGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 10
 ID ADD11315 standard; protein; 253 AA.
 AC ADD11315;
 DT 01-JAN-2004 (first entry)
 XX Human secreted/transmembrane PRO polypeptide #33.
 DE human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 KW endothelial cell tube formation.
 XX Homo sapiens.
 OS
 XX
 XX US2003105013-A1.
 PN
 XX
 PD 05-JUN-2003.
 XX
 XX 16-AUG-2002; 2002US-00223090.
 PF
 XX
 XX 20-JUN-2001; 2001WO-US019692.
 PR
 XX 09-JUL-2001; 2001WO-US021735.
 PR
 XX 20-FEB-2002; 2002US-00081056.
 XX
 XX (GETH) GENENTECH INC.
 PA
 XX Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX WPI; 2003-801242/75.
 DR N-PSDB; ADD11314.
 XX
 XX New isolated nucleic acid encoding a secreted and transmembrane
 PT polypeptide, useful for treating a cardiovascular, endothelial, or
 PT angiogenic disorder in a mammal, such as cancer or age-related macular
 PT degeneration.
 XX
 XX Claim 11; SEQ ID NO 66; 493pp; English.
 PS
 XX The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterised by the presence of
 CC an elevated level of FGF-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO1376 or PRO1449 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 XX Sequence 253 AA;
 SQ
 Alignment Scores:
 Pred. No.: 1,32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 7 Gaps: 0
 US-10-608-388A-1 (1-759) x ADD11315 (1-253)

QY 1 ATGGGCGAGTGGCGCATCCTCTCCAGACCGTGTGCTTCTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 QY 61 TGGGGGCGAGCTGGCATTTTATCTATGTGGAGCCCTATCTCTTCATCATCTTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 QY 121 TATGACCATCTCTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTATCATAGCTGTGA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
 QY 181 GGAACCTCTGCTTTTTCATCATTTGGGCTAAATTTGGTGTCTGCCCAATCCCGGAAAGTCGC 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 QY 241 TGTGGACTTCCACAGCTTTGTTCATCATCTCTCTCTGTTTGTTCACAGAAAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100
 QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGAAATGAGTTGATCGCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaIlysvaIcIuasnGluValAspArgSerIleGln 120
 QY 361 AAAGTGTATAAGACCTTACAAATGGAACCAACCTCATCTCTGCTAGCCGGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaIleAspTyr 140
 QY 421 GTACAGAGACGCTGCATCTTGTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
 QY 481 TGGTTCAAAAGAACCAACCAAGAGAGTCCCTCTTAGCTGCTGACAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATTTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGATGTGATCTGGGCGGCGACTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTTCAGCTGTGGCATGCTGTGTGCTTGCATCTGTGTGTCAGAAGGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
 QY 721 CCTGCTTACGAGCTCTCTCATCTGCGGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
 RESULT 11
 ADD37108
 ID ADD37108 standard; protein; 253 AA.
 AC ADD37108;
 XX
 XX
 XX 15-JAN-2004 (first entry)
 DT
 XX Human secreted/transmembrane PRO polypeptide #33.
 DE
 XX
 XX human; secreted protein; transmembrane protein; cardiovascular disorder;
 KW endothelial disorder; angiogenic disorder; myocardial infarction;
 KW cardiac hypertrophy; trauma; cancer; age-related macular degeneration;
 KW angiogenesis; endothelial cell apoptosis; smooth muscle cell growth;
 XX endothelial cell tube formation.
 OS Homo sapiens.
 XX
 XX US2003105012-A1.
 PN
 XX

PD 05-JUN-2003.
 XX
 PF 16-AUG-2002; 2002US-00223088.
 XX
 PR 15-SEP-2000; 2000US-0232887P.
 PR 20-JUN-2001; 2001WO-US019692.
 PR 09-JUL-2001; 2001WO-US021735.
 PR 20-FEB-2002; 2002US-00081056.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Ferrara N, Gerber H, Gerritsen ME, Goddard A;
 PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Stephan JF;
 PI Watanabe CK, Williams PM, Wood WI, Ye W;
 XX
 DR WPI: 2003-829354/77.
 DR N-PSDB; ADD37107.
 XX
 PT New isolated nucleic acids encoding a secreted and transmembrane
 PT polypeptide for treating a cardiovascular, endothelial, or angiogenic
 PT disorder in a mammal, such as cancer or age-related macular degeneration.
 XX
 PS Claim 11; SEQ ID NO 66; 492pp; English.
 XX
 CC The invention relates to an isolated nucleic acid encoding a secreted and
 CC transmembrane polypeptide (PRO). The nucleic acid, a polypeptide encoded
 CC by the nucleic acid, or an agonist or antagonist, is used to treat a
 CC cardiovascular, endothelial, or angiogenic disorder in a mammal,
 CC preferably a human. The human may have suffered a myocardial infarction
 CC or has cardiac hypertrophy, trauma, a cancer, or age-related macular
 CC degeneration. The cardiac hypertrophy is characterized by the presence of
 CC an elevated level of Pgf-2 alpha. A PRO polypeptide, given in the
 CC specification, or an agonist is used to inhibit or stimulate endothelial
 CC cell growth in a mammal. PRO21 or an agonist is used to induce cardiac
 CC hypertrophy. PRO137 or PRO149 is used to stimulate angiogenesis.
 CC PRO4302 or an agonist is used to induce endothelial cell apoptosis. A PRO
 CC polypeptide, given in the specification, or an agonist is used to
 CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
 CC cell tube formation. The present sequence represents the amino acid
 CC sequence of a PRO polypeptide of the invention.
 XX
 SQ Sequence 253 AA;
 Alignment Scores:
 Pred. No.: 1 32e-138 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 7 Gaps: 0
 US-10-608-388A-1 (1-759) x ADD37108 (1-253)
 QY 1 ATGGGCGAGTGGCGCATCACTCTCCAAAGACGGTGTCTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 QY 61 TGGGGGCGAGTGGCGATTTTATGCTATGTGGAGCGCTATGCTTCTCATCTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 QY 121 TATGACCACTCTTTCAGATGTCACAGCTCATCCCTGCTGTAGTCATAGCTGTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60
 QY 181 GGAGCCCTGCTTTTTCATCTATGGGCTAATGGCTGTGTGCCACAATCCGGAAAGTCG 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
 QY 241 TGTGACCTTGCACGTTTGTTCATCTCTGCTCTTGGTTTGTCTACAGAGTTGTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValValVal 100

QY 301 GTGGTTTGGGATATGTTTACAGAGCAAAAGGTGGAATAGAGTTGATCGCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
 QY 361 AAAGTGTATAAGACTTACCAATGGAACCAACCTGTAGTGTCTAGCCGGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
 QY 421 GTACGAGACAGCTGCATTGTTGTGAATTCAACTACTCTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 QY 481 TGGTTCAAAAGAAACCAAAACACAGAGTGTCCCTCTTGTAGTGTCTGCAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATGTATATGGAGCTGCGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAAGCTACAAGAAATCATGATGTCATGTCATGCGCCGACCTGGCATTTGCA 660
 Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTACAGTCTGCGCATGCTGTGTGCTTGCATGCTTGTGCAAGAGGAGTAGAGAT 720
 Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuLeuCysArgArgSerArgAsp 240
 QY 721 CTGCTTACGAGCTCTCTCATCATCTGCGGGAACCTATGCA 759
 Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
 RESULT 12
 ADD45736
 ID ADD45736 standard; protein; 253 AA.
 XX
 AC ADD45736;
 XX
 DT 29-JAN-2004 (first entry)
 XX
 DE Human Protein O60637, SEQ ID NO 11404.
 KW Human; pain; neuronal tissue; gene therapy;
 KW spinal segmental nerve injury; chronic constriction injury; CCI;
 KW spared nerve injury; SNI; Chung.
 XX Homo sapiens.
 OS
 PN WO2003016475-A2.
 XX
 PD 27-FEB-2003.
 XX
 PF 14-AUG-2002; 2002WO-US025765.
 XX
 PR 14-AUG-2001; 2001US-0312147P.
 PR 01-NOV-2001; 2001US-0346382P.
 PR 26-NOV-2001; 2001US-0333347P.
 XX
 PA (GEHO) GEN HOSPITAL CORP.
 XX
 PA (FARB) BAYER AG.
 XX
 PI Woolf C, D'urso D, Befort K, Costigan M;
 XX
 DR WPI; 2003-268312/26.
 DR GENBANK; O60637.
 XX
 PT New composition comprising two or more isolated polypeptides, useful for
 PT preparing a medicament for treating pain in an animal.
 XX
 PS Claim 1; Page; 1017pp; English.
 CC The invention discloses a composition comprising two or more isolated rat
 CC or human polynucleotides or a polynucleotide which represents a fragment,

CC polypeptide, given in the specification, or an agonist is used to
CC stimulate or inhibit smooth muscle cell growth, or to induce endothelial
CC cell tube formation. The present sequence represents the amino acid
CC sequence of a PRO polypeptide of the invention.

XX SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0

US-10-608-388A-1 (1-759) x ADE41316 (1-253)

QY 1 ATGGGCGAGTGGCGATCACCCTCTCCAAAGACCTGCTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGCGAGTGGCGATTTATGCTATGTGGAGCCTATGCTTCATCATCTATGATGAC 120
Db 21 TrpGlyAlaLaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCCTGCTGTAGTGATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleAlaVal 60
QY 181 GAGACCTCTTTTCATCATTTGGGCTAATTGGCTGTGCTGCCCAATCGGGAAAGTCG 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGAGTCCGAGTGTTCATCATCTCTGCTGCTTTGCTGCTGCTGCTGCTGCTGCTG 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGAAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAGACCTCAATAGGAACCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGAGACGTGCTATGTTGGATTCAGAAATTCACACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACCCAGAGTGTCCCTCTTAGCTGCTGACAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGACGCTGGGCCACCTCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGGCCGCTGCTGCTGCTGCTGCT 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACAGTGTGGGCGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CTGCTTTACAGCTCTCTCATCTACCTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253

RESULT 14

ADH43499

ID ADH43499 standard; protein; 253 AA.

XX

AC ADH43499;

XX DT 25-MAR-2004 (first entry)

XX DE Human PRO polypeptide #33.

XX KW Human; PRO; cardiovascular disorder; endothelial disorder;
XX KW angiogenic disorder; endothelial cell growth; cardiac hypertrophy;
XX KW cell apoptosis; cell tube formation; angiogenesis;
XX KW smooth muscle cell growth; myocardial infarction; trauma; cancer;
XX KW age-related macular degeneration; cytostatic; cardiant;
XX KW cerebroprotective; ophthalmological; vulnary.

OS Homo sapiens.

PN US2003224984-A1.

XX PD 04-DEC-2003.

XX PF 26-NOV-2002; 2002US-00305654.

XX PR 20-JUN-2001; 2001WO-US019692.

XX PA (GETH) GENENTECH INC.

XX PI Baker KP, Ferrara N, Gerber H, Gertitsen ME, Goddard A,
XX PI Godowski PJ, Gurney AL, Hillan KJ, Marsters SA, Pan J, Paoni NF;
XX PI Stephan JF, Watanabe CK, Williams PM, Wood WI, Ye W;

XX DR WPI; 2004-042166/04.

XX DR N-PSDB; ADH43498.

XX PT New PRO polypeptides and nucleic acids encoding the polypeptides, useful
XX PT for treating myocardial infarction, cardiac hypertrophy, trauma, cancer,
XX PT or age-related macular degeneration.

XX PS Claim 11; SEQ ID NO 66; 492pp; English.

XX CC The invention relates to human PRO polypeptides and the PRO
XX CC polynucleotides encoding them. The invention also relates to treating
XX CC cardiovascular, endothelial or angiogenic disorders in mammals,
XX CC inhibiting endothelial cell growth, stimulating endothelial cell growth,
XX CC inducing cardiac hypertrophy, cell apoptosis or cell tube formation and
XX CC stimulating angiogenesis or smooth muscle cell growth by administering
XX CC polypeptides of the invention. The PRO polypeptides and polynucleotides
XX CC are useful for treating cardiovascular, endothelial or angiogenic
XX CC disorders, e.g. myocardial infarction, cardiac hypertrophy, trauma,
XX CC cancer or age-related macular degeneration. The PRO polynucleotides are
XX CC useful as hybridisation probes in chromosome and gene mapping and in
XX CC generating antisense RNA and DNA, and for chromosome identification and
XX CC tissue typing. The PRO polypeptides and polynucleotides are also useful
XX CC in gene therapy and as molecular weight markers for protein
XX CC electrophoresis purposes. This sequence represents a human PRO
XX CC polypeptide of the invention.

XX SQ Sequence 253 AA;

Alignment Scores:

Pred. No.: 1.32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0

US-10-608-388A-1 (1-759) x ADH43499 (1-253)

QY 1 ATGGGCGAGTGGCGATCACCCTCTCCAAAGACCTGCTGCTTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

QY 61 TGGGGGCGAGTGGCGATTTATGCTATGTGGAGCCTATGCTTCATCATCTATGATGAC 120
|||||

```
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTCATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTCACCAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTGGCACGTTTGTTCATCATCTGCTCTCTGTTTGTTCACAGAAAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
Qy 301 GTGGTTTGGATATGTTTACAGACCAAGCTGGAAATGAGTTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAGTGTATAAGACCTCAATGGAAACCAACCTGTATGCTGTAGCCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaIleSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCTATTGTTGGAAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
Qy 481 TGGTTCAAAGAAACCAAAAACAGAGTGTCCCTCTTAGCTGCTGCGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTATGTCAGCTGGCCCAACCTTCCGACCTCTATGCTGAGGGGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAAGCTACAAAGAAATCATGATGCTGTATGCTGGCGCGCATGGCAATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
Qy 661 GCTATTACAGCTGGCGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyThrTyrAla 253
RESULT 15
ADJ75383
ID ADJ75383 standard; protein; 253 AA.
XX AC ADJ75383;
XX XX
XX 20-MAY-2004 (first entry)
XX DE Marker gene related amino acid sequence SEQ ID NO:635.
XX KW bronchial asthma; chronic obstructive pulmonary disease;
XX KW respiratory epithelial cell; interleukin-13; respiratory; antiasthmatic;
XX KW gene therapy; marker.
XX OS Homo sapiens.
XX XX
XX FN EPI394274-A2.
XX XX
XX PD 03-MAR-2004.
XX XX
XX PF 04-AUG-2003; 2003EP-00254857.
XX XX
XX PR 06-AUG-2002; 2002JP-00229312.
XX PR 20-MAR-2003; 2003JP-00077212.
XX XX
XX PA (GENO-) GENOX RES INC.
```

```
PI Ohtani N, Sugita Y, Yamaya M, Kubo H, Nagai H, Izuhara K;
XX WPI; 2004-193155/19.
XX
PT Testing for bronchial asthma or chronic obstructive pulmonary disease by
PT comparing the expression level of a marker gene in a biological sample
PT from a subject with the expression level of the gene in a sample from a
PT healthy subject.
XX
XX Example 11; SEQ ID NO 635; 241pp; English.
XX
XX The present invention describes a method of testing for bronchial asthma
XX or chronic obstructive pulmonary disease. The method comprises
XX determining the expression level of a marker gene in a biological sample
XX from a subject, comparing the expression level determined with the
XX expression level of the marker gene in a biological sample from a healthy
XX subject, and judging whether the subject has bronchial asthma or chronic
XX obstructive pulmonary disease. The marker gene comprises: (a) a group of
XX genes (S1) whose expression levels increase when respiratory epithelial
XX cells are stimulated with interleukin-13; or (b) a group of genes (S2)
XX whose expression levels decrease when respiratory epithelial cells are
XX stimulated with interleukin-13. Also described: (1) a reagent (I) for
XX testing for bronchial asthma or chronic obstructive pulmonary disease;
XX (2) a kit for screening for a candidate compound for a therapeutic agent
XX to treat bronchial asthma or chronic obstructive pulmonary disease; (3)
XX an animal model for bronchial asthma or chronic obstructive pulmonary
XX disease; (4) an inducer that induces bronchial asthma in a mouse; (5) a
XX method for producing an animal model for bronchial asthma or chronic
XX obstructive pulmonary disease; (6) a therapeutic agent for bronchial
XX asthma or chronic obstructive pulmonary disease, comprising the compound,
XX a marker gene or an antisense nucleic acid corresponding to a portion of
XX the marker gene, a ribozyme, a polynucleotide that suppresses the
XX expression of the gene through an RNAi effect or an antibody recognising
XX a protein encoded by a marker gene; and (7) a DNA chip for testing for
XX bronchial asthma or a chronic obstructive pulmonary disease, on which a
XX probe has been immobilised to assay a marker gene. (I) has respiratory
XX and antiasthmatic activities, and can be used in gene therapy. The method
XX is useful for testing for or screening for a therapeutic agent for
XX bronchial asthma or chronic obstructive pulmonary disease. The present
XX sequence is used in the exemplification of the present invention.
XX
XX Sequence 253 AA;
```

```
Alignment Scores:
Pred. No.: 1 32e-138 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 8 Gaps: 0
```

US-10-608-388A-1 (1-759) x ADJ75383 (1-253)

```
Qy 1 ATGGGCGCAGTGGCGCATCACCTCTCCAGACCGCTGCTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGCGACGTGGCATTTTATGCTATCTGGGACCTATGCTTTCATCACTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTCATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTCACCAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTGGCACGTTTGTTCATCATCTGCTCTCTGTTTGTTCACAGAAAGTTGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValValVal 100
```


QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGGAATAAGAGTTGATCGCAGCATTTGAG 360
Db |||||
QY 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Db |||||
QY 361 AAAGTGCTATAAGACCTACAAATGGAACCAACCTGATGCTGCTAGCCGGGCTATTGATTAT 420
Db |||||
QY 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Db |||||
QY 421 GTACAGACAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480
Db |||||
QY 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAAGAAACCAAAACCAAGAGTGTCCCTTTAGCTGTGTCAGAGAGACTGCCAGC 540
Db |||||
QY 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGGCAGCTGGCCCAACCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db |||||
QY 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db |||||
QY 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTTCAGCTGCTGGGCATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db |||||
QY 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACGAGCTCCTCATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 759
Db |||||
QY 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

Search completed: April 4, 2006, 21:24:08
Job time : 170 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:18:44 ; Search time 44.6 Seconds
(without alignments)
2401.327 Million cell updates/sec

Title: US-10-608-388a-1

Perfect score: 1429

Sequence: 1 atggggcagcgccgcatcac.....tccactggcggaacctatgca 759

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2166443 seqs, 705528306 residues

Total number of hits satisfying chosen parameters: 4332886

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=framet_n2p_model -DEV=xlip
-Q=/abss/ABSSWEB_spool/US10608388/runat_04042006_150648_14038/app_query.fasta 1
-DB=Uniprot -QFMT=fasta -SUFFIX=n2p.rup -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pf0 -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abss02p
-USER=US10608388 @CGN_1_1466 @runat_04042006_150648_14038 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Uniprot_05.80.*
1: uniprot_sprot.*
2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1336	93.5	253	1 TSN3 HUMAN	O60637 homo sapien
2	1336	93.5	253	2 Q5RE11_PONPY	O5re11 pongo pygma
3	1301	91.0	253	1 TSN3 MOUSE	O9qy33 mus musculus
4	1301	91.0	253	2 Q545I1_MOUSE	O545i1 mus musculus
5	1297	90.8	253	2 Q66H06_RAT	O66h06 rattus norv
6	1293	90.5	253	2 Q80XR4_MOUSE	O80xr4 mus musculus
7	1186	83.0	253	2 Q4V915_BRARE	O4v915 brachydanio
8	1165	81.5	253	2 Q4FZN3_XENLA	O4fnz3 xenopus lae
9	1147	80.3	253	2 Q5XH66_XENLA	O5xh66 xenopus lae
10	1140	79.8	253	2 Q4SAH7_TETNG	O4sah7 tetraodon n
11	1133	79.3	245	2 Q8BP2_MOUSE	O8bp2 mus musculus
12	1089	74.8	251	2 Q4SM43_TETNG	O4sm43 tetraodon n
13	607	42.5	271	2 Q4RLJ59_TETNG	O4rlj59 tetraodon n
14	599	41.9	243	2 Q6NWG0_BRARE	O6nwg0 brachydanio
15	527.5	36.9	240	2 Q6GP11_XENLA	O6gp11 xenopus lae
16	522.5	36.6	240	2 Q6P7J5_XENLA	O6p7j5 xenopus lae

17	430.5	30.1	245	2 Q5PQ10_XENLA	O5pq10 xenopus lae
18	370	25.9	252	2 Q5XJD1_BRARE	O5xjd1 brachydanio
19	367	25.7	256	2 Q4RS66_TETNG	O4rs66 tetraodon n
20	358.5	25.1	252	2 Q5Z1I8_CHICK	O5z1i8 gallus gall
21	358	25.1	237	2 Q6P2T9_BRARE	O6p2t9 brachydanio
22	344	24.1	253	1 CD151_MOUSE	O35566 mus musculus
23	343.5	24.0	244	1 TSN7_PANTR	O7yq10 pan troglod
24	343.5	24.0	244	2 Q723Z6_HUMAN	O723z6 homo sapien
25	343.5	24.0	249	1 TSN7_HUMAN	P41732 h tetraspan
26	342	23.9	253	1 CD151_RAT	O9qz86 rattus norv
27	338.5	23.7	254	2 Q6P031_BRARE	O6p031 brachydanio
28	338	23.7	253	2 Q921J7_MOUSE	O921j7 mus musculus
29	337	23.6	253	2 Q6DDI3_XENLA	O6ddi3 xenopus lae
30	336	23.5	236	1 CD63_BOVIN	O9xsk2 bos taurus
31	335.5	23.5	249	2 Q4RS43_MACFA	O4rs43 macaca fasc
32	335	23.4	253	1 CD151_CERAE	P61170 cercopithec
33	335	23.4	253	1 CD151_MACMU	P61171 macaca mula
34	334.5	23.4	244	2 Q6PDN6_MOUSE	O6pdn6 mus musculus
35	334.5	23.4	249	1 TSN7_MOUSE	O62283 mus musculus
36	333.5	23.3	245	1 TSN6_HUMAN	O43657 homo sapien
37	333.5	23.3	245	1 TSN6_MOUSE	O70401 mus musculus
38	333.5	23.3	245	2 Q6TAN9_HUMAN	O6tan9 homo sapien
39	333.5	23.3	245	2 Q54A42_HUMAN	O54a42 homo sapien
40	333.5	23.3	245	2 Q99L96_MOUSE	O99l96 mus musculus
41	333.5	23.3	285	2 Q59ED5_HUMAN	O59ed5 homo sapien
42	332.5	23.3	244	1 TSN7_PONPY	O7yqk9 pongo pygma
43	332.5	23.3	245	2 Q5RA55_PONPY	O5ra55 pongo pygma
44	332.5	23.3	246	2 Q5R515_PONPY	O5r515 pongo pygma
45	332	23.2	253	2 Q53FU5_HUMAN	O53fu5 homo sapien

ALIGNMENTS

RESULT 1
TSN3_HUMAN
ID TSN3 HUMAN STANDARD; PRT; 253 AA.
AC O60637; Q9BW22; Q9NVX9;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 13-SEP-2005 (Rel. 48, Last annotation update)
DE Tetraspanin-3 (Tspan-3) (Transmembrane 4 superfamily member 8)
DE (Tetraspanin TM4-A).
GN Name=TSN3; Synonyms=TM4SP8;
OS Homo sapiens (Human)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Hominidae;
OC Homo.
OX NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE [MRNA].
RX MEDLINE=98390278; PubMed=9714763; DOI=10.1016/S0167-4781(98)00087-6;
RA Todd S.C., Doctor V.S., Levy S.;
RT "Sequences and expression of six new members of the tetraspanin/TM4SF family";
RL Biochim. Biophys. Acta 1399:101-104(1998).
RN [2]
RP NUCLEOTIDE SEQUENCE [MRNA].
RA Puls K.I., Ni J., Liu D., Morahan G., Wright M.D.;
RT "The molecular characterization of four tetraspanins";
RN [3]
RP NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
RX PubMed=14702039; DOI=10.1038/ng1285;
RA Ota T., Suzuki Y., Nishikawa T., Otsuki T., Sugiyama T., Irie R.,
RA Wakamatsu A., Hayashi K., Sato H., Nagai K., Kimura K., Makita H.,
RA Sekine M., Ohyashiki M., Nishi T., Shibahara T., Tanaka T., Ishii S.,
RA Yamamoto J.-I., Saito K., Kawai Y., Isono Y., Nakamura Y.,
RA Nagahari K., Murakami K., Yasuda T., Iwayanagi T., Wagatsuma M.,
RA Shiratori A., Sudo H., Hosoiri T., Kaku I., Kodaira H., Kondo H.,
RA Sugawara M., Takahashi K., Kanda K., Yokoi T., Furuya T., Kikkawa E.,
RA Omura Y., Abe K., Kamihara K., Katsuta N., Sato K., Tanikawa M.,
RA Yamazaki M., Ninomiya K., Ishibashi T., Yamashita H., Murakawa K.,
RA Fujimori K., Tanai H., Kimata M., Watanabe M., Hiraoaka S., Chiba Y.,

RA Ishida S., Ono Y., Takiguchi S., Watanabe S., Yosida M., Hotuta T.,
 RA Kusano J., Kanehori K., Takahashi-Fujii A., Hara H., Tanase T.-O.,
 RA Nomura Y., Togiya S., Komai F., Hara R., Takeuchi K., Arita M.,
 RA Imose N., Mueashino K., Yuuki H., Oshima A., Sasaki N., Aotsuka S.,
 RA Yoshikawa Y., Matsunawa H., Ichihara T., Shiohata N., Sano S.,
 RA Moriya S., Momiya N., Satoh N., Takami S., Terashima Y., Suzuki O.,
 RA Nakagawa S., Senoh A., Mizoguchi H., Goto Y., Shimizu F., Wakebe H.,
 RA Hishigaki H., Watanabe T., Sugiyama A., Takemoto M., Kawakami B.,
 RA Yamazaki M., Watanabe K., Kumagai A., Itakura S., Fukuzumi Y.,
 RA Fujimori Y., Komiyama M., Tashiro H., Tanigami A., Fujiwara T.,
 RA Ono T., Yamada K., Fujii Y., Ozaki K., Hirao M., Ohmori Y.,
 RA Kawabata A., Hikiji T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Oktani R., Kawakami T., Noguchi S., Itoh T., Shigeta K., Senba T.,
 RA Matsumura K., Nakajima Y., Mizuno T., Morinaga M., Saeki M.,
 RA Togashi T., Oyama J., Hata H., Watanabe M., Komatsu T.,
 RA Muzushima-Sugano J., Satoh T., Shirai Y., Takahashi Y., Nakagawa K.,
 RA Okumura K., Nagase T., Nomura N., Kikuchi H., Masuho Y., Yamashita R.,
 RA Nakai K., Yada T., Nakamura Y., Ohara O., Isogai T., Sugano S.,
 RT "Complete sequencing and characterization of 21,243 full-length human
 RT cDNAs";
 RL Nat. Genet. 36:40-45(2004).
 [4]
 RN NUCLEOTIDE SEQUENCE [LARGE SCALE MRNA].
 RP TISSUE=Cervix, Colon, Muscle, and Skin;
 RC MEDLINE=2238257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins P.S., Wagner L., Shellen C.W., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.P., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S.K., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettner M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -!- FUNCTION: Regulates the proliferation and migration of
 CC oligodendrocytes, a process essential for normal myelination and
 CC repair (By similarity).
 CC -!- SUBUNIT: Interacts with claudin 11 and integrins (By similarity).
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -!- SIMILARITY: Belongs to the tetraspanin (TM4SF) family.
 CC -----
 CC This Swiss-Prot entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC European Bioinformatics Institute. There are no restrictions on its
 CC use as long as its content is in no way modified and this statement is not
 CC removed.
 CC -----
 DR EMBL; AF054840; AAC69716.1; -; mRNA.
 DR EMBL; AF133423; AAF08362.1; -; mRNA.
 DR EMBL; AK001326; BAA91627.1; -; mRNA.
 DR EMBL; AK001305; BAA91613.1; -; mRNA.
 DR EMBL; AK001310; BAA91615.1; -; mRNA.
 DR EMBL; BC000704; AAH00704.1; -; mRNA.
 DR EMBL; BC004280; AAH04280.1; -; mRNA.
 DR EMBL; BC009248; AAH09248.1; -; mRNA.
 DR EMBL; BC011206; AAH11206.1; -; mRNA.
 DR PIR; A59264; A59264.
 DR Ensembl; ENSG00000140391; Homo sapiens.
 DR HGNC; HGNC:17752; TSPAN3.
 DR H-InvDB; HIX0012461; -.
 DR GO; GO:0016021; C:integral to membrane; TAS.
 DR InterPro; IPR000301; Transmem_4.

DR PFam; PF00335; Tetraspannin; 1.
 DR PRINTS; PR00259; TMFOUR.
 DR PROSITE; PS00421; TM4_1; 1.
 KW Glycoprotein; Transmembrane.
 FT TOPO_DOM 1 11 Cytoplasmic (Potential).
 FT TRANSMEM 12 32 Potential.
 FT TOPO_DOM 33 50 Extracellular (Potential).
 FT TRANSMEM 51 71 Potential.
 FT TOPO_DOM 72 85 Cytoplasmic (Potential).
 FT TRANSMEM 86 106 Potential.
 FT TOPO_DOM 107 212 Extracellular (Potential).
 FT TRANSMEM 213 233 Potential.
 FT TOPO_DOM 234 253 Cytoplasmic (Potential).
 FT CARBOHYD 127 127 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 152 152 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 167 167 N-linked (GlcNAc...) (Potential).
 FT CARBOHYD 183 183 N-linked (GlcNAc...) (Potential).
 FT CONFLICT 85 85 Missing (in Ref. 4; AAH00704).
 FT CONFLICT 236 236 R -> G (in Ref. 3; BAA91613).
 SQ SEQUENCE 253 AA; 28018 MW; E074A4CD57229EC6 CRC64;
 Alignment Scores:
 Pred. No.: 2,296-121 Length: 253
 Score: 1336.00 Matches: 253
 Percent Similarity: 100.0% Conservative: 0
 Best Local Similarity: 100.0% Mismatches: 0
 Query Match: 93.5% Indels: 0
 DB: 1 Gaps:
 US-10-608-388a-1 (1-759) x TSN3_HUMAN (1-253)
 QY 1 ATGGGGCAGTGGCGCATCCTCTCCAGACCGCTGCTGGTCTTTCTCAACCTCATCTTC 60
 Db 1 MetGlyGlnCysGlyIleThrSerSerIleThrValLeuValPheLeuAsnLeuIle 20
 QY 61 TGGGGGCGACGTGGCATTATGCTATGTGGAGCCCTATGCTTCATCCTATGATGAC 120
 Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAsp 40
 QY 121 TATGACCACTCTTTGAAGATGTACACCTCATCCTGCTGCTAGTGATCATGCTCTA 180
 Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValIleAlaVal 60
 QY 181 GGAGCCCTGCTTTTCATCTATGGGCTAATTTGGCTGTGTGCCAATCCGGAAGTCGC 240
 Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysAlaThrIleArgGluSerArg 80
 QY 241 TGTGGACTGCCAGTGTGTCATCATCTGCTCTTGGTTTGTGTCAGAAAGTTGTTGTA 300
 Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuValPheValThrGluValVal 100
 QY 301 GTGGTTTGGATATGTTTACAGAGCAAGGTGGAATGAGTTGATCGCAGCATTCAG 360
 Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIle 120
 QY 361 AAAGTGTATAGACTCAATGGAACCAACCTGATGCTAGCCGGGCTATTGATTAT 420
 Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAsp 140
 QY 421 GTACAGAGACAGTGCATTTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGAT 480
 Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
 QY 481 TGGTTCAGAGAAACCAAAACAGAGTGCTCCCTCTTAGCTCTGCAGAGAGACTGCCAGC 540
 Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
 QY 541 AATTGTAATGGCAGCTGGCCACCTTCCACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGATGATCTCTGGGCGGCACTGGCATTTGCA 660

25-OCT-2004 (TREMBlrel. 28, Last annotation update)
DE Transmembrane 4 superfamily member 8.
GN Name=Tm4sf8;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
EC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Testis;
RA Director MGC Project;
RA Submitted (SEP-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC082102; AAH82102.1; -; mRNA.
DR GO; GO:0016021; C: integral to membrane; IEA.
DR InterPro; IPR000301; Transmem 4.
DR Pfam; PF00335; Tetraspanin; 1.
DR PRINTS; PR00259; TMFOUR.
DR PROSITE; PS00421; TM4_1; 1.
KW Transmembrane.
SQ SEQUENCE 253 AA; 28094 MW; 26B85FDDAF82ED8D CRC64;

Alignment Scores:
Pred. No.: 1.48e-117 Length: 253
Score: 1297.00 Matches: 245
Percent Similarity: 98.4% Conservative: 4
Best Local Similarity: 96.8% Mismatches: 4
Query Match: 90.8% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x Q6H06_RAT (1-253)

QY 1 ATGGSCCAGTGGGACATCCCTCCCAAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyLeuThrSerSerlysthrValLeuValPheLeuAsnLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGCATTTTATGCTATGTGGGAGCCTATGCTTCATCATTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
QY 121 TATGACCACTTCTTTGAAGATGTGACAGCTATCCCTGCTGTAGTCATCATCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuPheProAlaValValIleMetAlaVal 60
QY 181 GGAGCCCTCTTTTCATCATTTGGGCTAATGGCTGCTGTGCACATCCGGGAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGGACTTGGCACCGTTGTGTCATCATCTCTGCTCTTGGTTTGTGCACAGAAGTTGTGTA 300

Db 81 CysGlyLeuAlaThrPheValPheIleLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGCAAAATGAGGTGATCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaValValGluAsnGluAlaAspArgSerIleGln 120
QY 361 AAAGTGATTAAGACCTCAATAGGAACCAACCTGCTGCTAGCCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnSerAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGGGAAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTyrGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACCCAGAGTGCTCTTCTAGCTGCTCAGACAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaArg 180
QY 541 AATTGTAAATGGCAGCTGGCCCAACCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 SerCysAsnGlySerLeuAlaAsnProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGACTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 660
Db 201 ValValLysLysLeuGlnGluLeuLeuMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCATTTCAGCTGCTGGGCATGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgSerArgAsp 240
QY 721 CCTGCTTACAGCTCTCTCATCATCTGGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 6
Q80XR4 MOUSE
ID Q80XR4 MOUSE PRELIMINARY; PRT; 253 AA.
AC Q80XR4;
DT 01-JUN-2003 (TREMBlrel. 24, Created)
DT 01-JUN-2003 (TREMBlrel. 24, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Tetraspanin 3.
GN Name=Tspan3; Synonyms=Tm4sf8;
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RC TISSUE=Brain;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalish D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

QY 541 AATTGTAATGACGAGCTGGCCACCCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 DB 181 AsnCysThrGlySerMetAsnLysProGluAspLeuTyrSerGluGlyCysGluAlaLeu 200
 QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATCATGCTGCGCGGCACTGGCATTTTGA 660
 DB 201 ValValGluLysLeuGlnGluMetMetTyrValIleTyrAlaLeuAlaPheAla 220
 QY 661 GCTATTGAGCTGCTGGGCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 221 ThrIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgThrArgAsp 240
 QY 721 CCTGCTTACGAGCTCCTCATCTGCGGGAACCTATGCA 759
 DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 9
 Q5XH66_XENLA
 ID Q5XH66_XENLA PRELIMINARY; PRT; 253 AA.
 AC Q5XH66;
 DT 25-OCT-2004 (TrEMBLrel. 28, Created)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE LOC495251 protein.
 GN Names=LOC495251;
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipiloidea; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative".
 RL Dev. Dyn. 225:384-391(2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udwin T.B., Toshivuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Halle S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickinson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalek U., Smailus D.E.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences".
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Ovary;
 RA Klein S., Gerhard D.S.;
 RL Submitted (OCT-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC084207; AA84207.1; -, mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspanin; I.

DR PRINTS; PRO0259; TMFOUR.
 DR PROSITE; PS00421; TM4.1.1.
 SQ SEQUENCE 253 AA; 28067 MW; F29C6C4E7BCF6C18 CRC64;

Alignment Scores:
 Pred. No.: 6,66e-103 Length: 253
 Score: 1147.00 Matches: 212
 Percent Similarity: 90.5% Conservative: 17
 Best Local Similarity: 83.8% Mismatches: 24
 Query Match: 0.3% Indels: 0
 DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x Q5XH66_XENLA (1-253)

QY 1 ATGGGCGAGTGGGCACTCCTCCCAAGACCGTCTGCTCTTCTCAACCTCATCTTC 60
 DB 1 MetGlyGlnCysGlyLeuIleSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
 QY 61 TGGGGGCGAGCTGGCAATTTTATGCTATGTGGGAGCCATGTCTTCATCATGTATGAC 120
 DB 21 TrpAlaAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
 QY 121 TATGACCACTTCTTGAAGATGTACACGCTCATCCCTGCTGTAGTATGATCATAGCTGA 180
 DB 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProGlyValIleIleAlaAla 60
 QY 181 GGAGCCCTGCTTTTCATCATCTGGGCTAATGCTGCTGTGCCACAATCCGGGAAGTCG 240
 DB 61 GlyThrLeuLeuPheValIleGlyLeuIleGlyCysAlaThrIleArgGluSerHis 80
 QY 241 TGTGGACTTGGCCACGTTTTCATCTCCTCTGCTCTTGTGTTTGTGCACAGAAGTTGTGA 300
 DB 81 CysGlyLeuAlaThrPheValValIleLeuLeuValPheValThrGluValVal 100
 QY 301 GTGGTTTGGGATATGTTTACAGAGCAAGGTGGAAAATAGAGTTGATCGCAGCATTCAG 360
 DB 101 ValValLeuGlyTyrIleTyrArgAlaValGluAspGluValAspAsnThrIleAla 120
 QY 361 AAAGTGTATAAGACCTTACAACTGACCAACCTGATGCTGTAGCCGGCTATTGATTAT 420
 DB 121 AsnValPheAsnGlnTyrAsnGlyIleSerProAspSerAlaSerArgAlaIleAspTyr 140
 QY 421 GTACAGAGACAGCTGCATTGTTGTGAATTCACACTACTCTCAGACTGGGAAAATACAGAT 480
 DB 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTyrGluAsnThrPro 160
 QY 481 TGGTTCAAGAAACCAAAACCAAGTGTCCCTCTTAGCTGTGCTGAGAGAGACTGCCAGC 540
 DB 161 TrpPheSerGluAlaLysAsnAsnSerValProLeuSerCysCysArgAsnTyrValPhe 180
 QY 541 AATTGTAATGCGAGCTGGCCACCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 DB 181 AsnCysThrGlySerMetAsnLysProAlaAspLeuTyrSerGluGlyCysAlaLeu 200
 QY 601 GTAGTGAAGAGCTACAAAGAAATCATGATGCTATGTGCTGCGCGGCACTGGCATTTTGA 660
 DB 201 ValValGluLysLeuGlnGluMetMetTyrValIleTyrAlaAlaLeuAlaPheAla 220
 QY 661 GCTATTGAGCTGCTGGGCACTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 720
 DB 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaPheIleValLeuValLeuValLeuValLeu 240
 QY 721 CCTGCTTACGAGCTCCTCATCTGCGGGAACCTATGCA 759
 DB 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253

RESULT 10
 Q4SAH7_TETNG
 ID Q4SAH7_TETNG PRELIMINARY; PRT; 253 AA.
 AC Q4SAH7;
 DT 13-SEP-2005 (TrEMBLrel. 31, Created)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last sequence update)
 DT 13-SEP-2005 (TrEMBLrel. 31, Last annotation update)

Chromosome 5 SCAF14685, whole genome shotgun sequence.
(Fragment).
ORFNames=GSTENG00021449001;
OS Tetraodon nigroviridis (Green puffer).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
OC Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;
OC Tetraodontidae; Tetraodontidae; Tetraodon.
OX NCBI_TaxID=99883;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Jallion O., Aury J.M., Brunet F., Petit J.L., Stange-Thomann N.,
RA Mauceli E., Bouneau L., Fischer C., Ozouf-Costaz C., Bernot A.,
RA Nicaud S., Jaffe D., Fisher S., Lutfalla G., Dossat C., Segurens B.,
RA Da Silva C., Salanoubat M., Levy M., Boudet N., Castellano S.,
RA Anthouard V., Jubin C., Castelli V., Katinka M., Vacherie B.,
RA Biemont C., Skalli Z., Cattolico L., Poulain J., De Berardinis V.,
RA Cruaud C., Duprat S., Bottier P., Coutanceau J.P., Gouzy J.,
RA Parra G., Lardier G., Chapelle C., McKernan K.J., McEwan P., Bosak S.,
RA Kellis M., Wolff J.N., Guigo R., Zody M.C., Mesirov J.,
RA Lindblad-Toh K., Birren B., Nusbaum C., Kahn D., Robinson-Rechavi M.,
RA Laudet V., Schachter V., Quetier F., Saurin W., Scarpelli C.,
RA Wincker P., Lander E.S., Weissenbach J., Roest Crolius H.,
RA "Genome duplication in the teleost fish Tetraodon nigroviridis reveals
RT the early vertebrate proto-karyotype.";
RL Nature 431:946-957(2004).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RG Genoscope; Whitehead Institute Centre for Genome Research;
RL Submitted (FEB-2004) to the EMBL/GenBank/DBJ databases.
CC -!- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; CAAG01014685; CAG023355.1; -; Genomic_DNA.
FT NON TER 253
SQ SEQUENCE 253 AA; 28209 MW; 08DA70B97B59C591 CRC64;

Alignment Scores:
Pred. No.: 3,22e-102 Length: 253
Score: 1140.00 Matches: 209
Percent Similarity: 90.5% Conservative: 20
Best Local Similarity: 82.6% Mismatches: 24
Query Match: 79.8% Indels: 0
DB: 2 Gaps: 0

US-10-608-388a-1 (1-759) x QASAH7_TETNG (1-253)

Qy 1 ATGGGCCAGTGGCGGATCACCTCTCTCAAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyLeuThrSerSerGlyThrValLeuValPheLeuAsnLeuilePhe 20

Qy 61 TGGGGGGGAGTGGGATTTATGCTATGTTGGGAGGCTATGCTTCATCATCTATGATGAC 120
Db 21 TrrpAlaAlaAlaGlyIleLeuLeuGlyLeuLeuGlyAlaThrValPheileThrTyrAspAsp 40

Qy 121 TATGACCACTCTTTGAGATGCTGTACAGCTCATCCCTGCTGTAGTGTATGATCATCTCTA 180
Db 41 TyrAspHisPhePheGluAspValThrLeuileProAlaVallellelleAlaVal 60

Qy 181 GGAGCGCTCTTTTCATCTGGGCTATATGCTGCTGTGCCACATCGGGAAGTGGC 240
Db 61 GlyThrLeuLeuPheilelleGlyLeuileGlyCysAlaThrileArgGluSerSer 80

Qy 241 TGTGACCTGGCAGTGGTTCATCATCTCTGCTCTTGGTGGTGGTGGTGGTGGTGGTGGT 300
Db 81 CysGlyLeuAlaThrPheAlaAlaAlaLeuLeuLeuValPheAlaThrGluCysValVal 100

Qy 301 GTGGTTTGGGATGTTTACAGACCAAGGTTGAAATGAGTTGATCGGAGCATTCAG 360
Db 101 ValValLeuGlyTyrileThrArgAlaValGluAspGluValAsnHisSerileGln 120

Qy 361 AAAGTGTATAGACCTACATCGAATCGAACCTGATGCTGTAGCGGGCTATTGATTAT 420
Db 1 Nature 409:685-690(2001).

Db 121 LysValTyrAsnGluTyrAsnGlyThrAsnSerAspAlaProSerArgAlaileAspTyr 140
Qy 421 GTACAGACAGCTGCATTTCTTGGGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrrpArgAsnThrArg 160
Qy 481 TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGCTGCAGACAGACTGCCAGC 540
Db 161 TrpPheLysGluSerArgAsnSerValProValSerCysGlnProSerIleSer 180

Qy 541 AATTGTAAATGGAGCTGGCCACCTTCGACCTCTATGCTAGGGGTGTGAGCTCTA 600
Db 181 AsnCysThrGlyThrLeuAlaArgProSerGluLeuTyrGlnGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAAGCTACAGAAATCATGATGATGCTGTGCTGTGCTGTGCTGTGCTGTGCT 660
Db 201 ValValLysLysLeuLysGluileMetMetTyrValleThrAlaAlaLeuThrPheAla 220
Qy 661 GCTATTGAGTGTGGGCTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCTGTGCT 720
Db 221 SerileGlnMetLeuGlyMetLeuCysAlaCysValValLeuLeuCysArgArgThrHisAsp 240
Qy 721 CTGTCTTACAGCTCTCTCATCATCTGCGGAGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuValThrThrAsnSerTyrAla 253

RESULT 11
Q8BPV2_MOUSE
ID Q8BPV2_MOUSE PRELIMINARY; PRT; 245 AA.
AC Q8BPV2;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
DE Mus musculus 0 day neonate eyeball cDNA, RIKEN full-length enriched
DE library, clone: E13009003 product: transmembrane 4 superfamily member
DE 8, full insert sequence.
GN Name=Tspan3; Synonyms=Tm4sf8;
OS Mus musculus (Mouse)
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
OC Muroidea; Muridae; Murinae; Mus.
RN NCBI_TaxID=10090;
RP [1]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=EyeBall;
RX MEDLINE=9279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA "High-efficiency full-length cDNA cloning.";
RL Meth. Enzymol. 303:19-44(1999).
RN [2]
RP NUCLEOTIDE SEQUENCE.
RC STRAIN=C57BL/6J; TISSUE=EyeBall;
RX MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aizawa K., Iwata M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikolaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Stauble P., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombares P.,
RA Nordone P., Ring B., Schenwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

Db 220 PhePheGlyMetLeuSerValCysValIleThrCysLysSerLysLysAsnGluTyrGln 239
 QY 721 CTGCTTAC 729
 Db 240 ProLeuTyr 242
 RESULT 15
 Q6GP11_XENLA PRELIMINARY; PRT; 240 AA.
 AC Q6GP11;
 DT 05-JUL-2004 (TREMBLrel. 27, Created)
 DT 05-JUL-2004 (TREMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TREMBLrel. 27, Last annotation update)
 DE MGC80751 protein.
 GN Name=MGC80751; (African clawed frog).
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
 OC Xenopodinae; Xenopus; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko M., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stabileton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Lomuellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Whiting M., Madan A., Kettman M., Madan A., Rodrigues S., Sanchez A.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalilus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
 RN [2]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative.";
 RL Dev. Dyn. 225:384-391 (2002).
 RN [3]
 RP NUCLEOTIDE SEQUENCE.
 RC TISSUE=Spleen;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUN-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC073338.1; -, mRNA.
 DR GO; GO:0016021; C:integral to membrane; IEA.
 DR InterPro; IPR000301; Transmem 4.
 DR Pfam; PF00335; Tetraspannin; I.
 DR PRINTS; PRO0259; TMFOUR.
 SQ SEQUENCE 240 AA; 26875 MW; 96475F0A8F920998 CRC64;

Alignment Scores:

Pred. No.:	2,19e-42	Length:	240
Score:	527.50	Matches:	89
Percent Similarity:	62.8%	Conservative:	61
Best Local Similarity:	37.2%	Mismatches:	84
Query Match:	36.9%	Indels:	5
DBs:	2	Gaps:	3

US-10-608-388A-1 (1-759) x Q6GP11_XENLA (1-240)

QY 22 TCCTCCAGACCGTCTGCTCTTCTCAACTCATCTTCTGGGGGACGCTGGCATTTTA 81
 Db 7 ThrSerLysThrPheLeuPheLeuValSerLeuIlePheLeuAlaAlaSerValGlyLeu 26
 QY 82 TGCTATGTGGAGGCTATGCTTCATCAGTATGACTATGACCTATGACCTATCTTTGAAGAT 141
 Db 27 AlaTyrValGlyIleSerThrIleValThrTyrLysGlnTyrGluAspLeuGlyAsn 46
 QY 142 GTGTACAGCTCATCCCTGCTGTAGTATGATCATAGCTGTAGGAGCCCTGCTCTTTCATCAT 201
 Db 47 MetTyrValMetLeuProSerValIleLeuLeuAlaIleValValMetPhePheIle 66
 QY 202 GGGCTAATTGGCTGCTGCGCACAAATCGGGAAGTGCCTGTGACCTTGCCACGTTTGTG 261
 Db 67 AlaIleLeuGlyCysSerThrThrGlnGluSerCysGlyLeuGlyCysPheMet 86
 QY 262 ATCATCTGCTCTTGGTGTTCACAGAAAGTTGTGTGTAGTGGTGTGGGATATGTTTAC 321
 Db 87 PheLeuIleSerIleIlePheAlaAlaGlyValAlaAlaIleIleLeuGlyLeuValTyr 106
 QY 322 AGACGAAGGTGGAAATAGAGGTGTATCGCAGCATTCAGAAAGTGTATAGACCTACAT 381
 Db 107 ValAsnLysIleAsnProGluLeuGluLysAsnMetAspAsnLeuTyrLysLysTyrSer 126
 QY 382 GGAACCAACCTGATGCTGTAGCCGGCTATTGATTATGTATACAGACAGACGCTGCTTGT 441
 Db 127 GlyAla-----AspValGlnSerSerThrValAspPheIleGlnGluLeuGlnCys 144
 QY 442 TGTGGAATTCACAACTACTCAGACTGGGAAATACAGATTGTTTCAAGAAACCAAAAC 501
 Db 145 CysGlyArgLysAsnTyrThrAspTyrGluThrAspTyrTyrLys-----AsnAsn 162
 QY 502 CAGAGTGTCCCTCTTAGCTGTGAGAGAGACTCCAGCAATTGTAATGGCAGCTGSCC 561
 Db 163 LysSerLeuProLeuSerCysCysLysLysAsnAlaGlnAspCysGlnArgValIleGly 182
 QY 562 CACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAAGCTACAAGAA 621
 Db 183 GlnIleLysAspIleTyrThrGluGlyCysGluProLysLeuGluThrLeuIleHisGln 202
 QY 622 ATCATGATGATGTATCTGCGCGCCTGCGCATTTGCGACTATTCAGCTATTCAGCTGCGGCATG 681
 Db 203 ValLeuArgTyrSerMetPheValIleLeuGlyPheAlaIleValGluLeuPheAlaMet 222
 QY 682 CTGTGTGCTTCATCGTGTGTGAGAGAGAGATCGCTGCTTACAGCTCTCTC 738
 Db 223 IleSerMetCysValIleSerCysArgProAlaArgHis---ThrTyrHisLeuLeu 240

Search completed: April 4, 2006, 21:31:38
 Job time : 230 secs

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:24:24 ; Search time 8.1 Seconds
(without alignments)
1803.173 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atggcgccagcgcgccatcac.....tccactggcggaacctatgca 759

Scoring table: BLOSUM62

Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 566832

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+_{n2p}.model -DEV=xlip
-Q=/abss/ABSSWEB_spool/US10608388/runat_04042006_150651_14080/app_query.fasta_1
-DB=PIR -QMT=fastan -SUFFIX=n2p.rpr -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bites -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388_@CGN_1_1_63 @runat_04042006_150651_14080 -NCPUS=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOPEXT=7
-YGAPOPEXT=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

PIR_80.*
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1336	93.5	253	2 A59264	tetraspan TSPAN-3
2	343.5	24.0	244	1 I39368	T-cell acute lymph
3	333.5	23.3	245	2 A59258	tetraspan TSPAN-6
4	333.5	23.3	245	2 A59260	tetraspan TSPAN-6
5	330.5	23.1	238	1 S43511	CD63/ME491 antigen
6	328.5	23.0	238	1 A46508	CD63/ME491 antigen
7	322.5	22.6	238	1 JC2297	CD63 antigen - rab
8	301.5	21.1	238	2 A59265	tetraspan TSPAN-4
9	297.5	20.8	238	1 I38016	melanoma-associate
10	283	19.8	267	1 A46493	metastasis suppress
11	273.5	19.1	219	1 A37243	hemopoietic cell s
12	263	18.4	241	2 A59262	tetraspan TSPAN-1
13	259.5	18.2	219	1 A39574	leukocyte antigen
14	259.5	18.2	266	2 I49561	C33/R2/IA4 - mouse

15	257.5	18.0	281	1 B47629	cell surface glyco
16	251	17.6	218	1 A40181	23K integral membr
17	251	17.6	237	1 A36056	tumor-associated a
18	250.5	17.5	282	2 T21896	hypothetical prote
19	242.5	17.0	281	1 A47629	cell surface glyco
20	235	16.4	218	1 A43522	23K integral membr
21	222.5	15.6	226	1 JX0221	CD9 antigen - bovi
22	218.5	15.3	226	1 S39262	CD9 antigen - rat
23	218.5	15.3	226	1 I49589	antigen - mouse
24	218.5	15.3	228	1 A40402	CD9 antigen (valid
25	215.5	15.1	228	1 A42929	CD9 antigen - gree
26	210	14.7	206	2 T25161	hypothetical prote
27	207.5	14.5	236	1 A46472	cell surface prote
28	205	14.3	222	2 A59263	tetraspan TSPAN-2
29	201.5	14.1	236	1 A35649	cell surface prote
30	196	13.7	308	2 T24912	hypothetical prote
31	183.5	12.8	264	2 A59261	tetraspan TSPAN-5
32	182.5	12.8	194	2 T25548	hypothetical prote
33	174	12.2	233	2 T15620	hypothetical prote
34	171	12.0	359	2 T18667	hypothetical prote
35	164	11.5	427	2 T32852	hypothetical prote
36	159	11.1	321	2 T45053	hypothetical prote
37	155.5	10.9	242	2 T15361	hypothetical prote
38	153	10.7	203	2 T22537	hypothetical prote
39	151.5	10.6	351	2 I54347	rod outer segment
40	149	10.4	258	2 I46080	uroplakin Ia - bov
41	143	10.0	260	2 A41531	TGFbeta-regulated
42	138	9.7	172	2 T28914	hypothetical prote
43	137	9.6	260	2 I46081	uroplakin Ib - bov
44	137	9.6	702	2 T34313	hypothetical prote
45	133.5	9.3	366	2 T22544	hypothetical prote

ALIGNMENTS

RESULT 1

A59264
tetraspan TSPAN-3 - human
C;Species: Homo sapiens (man)
C;Date: 13-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59264
R;Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TW4SF family.
A;Reference number: A59258; MUID:98390278; PMID:9714763
A;Accession: A59264
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-253 <TOD>
A;Cross-references: UNIPROT:O60637; UNIPARC:UPI0000048A5D; GB:AF054840; NID:G2997744;
C;Genetics:
A;Gene: TSPAN-3
C;Superfamily: CD9 antigen

Alignment Scores:
Pred. No.: 4.39e-118 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservatives: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 2 Gaps: 0

US-10-608-388A-1 (1-759) x A59264 (1-253)

QY	1	ATGGGCGCAGTGGCGCATCCCTCCCAAGACCGTGTCTCTTCTCAACCTCATCTTC	60
DB	1	MetGlyGlnCysGlyIleThrSerLyThrValLeuValPheLeuLeuLeuPhe	20
QY	61	TGGGGGGCGAGCTGGCGATTTATGCTATGTGGGAGCCTATGTCTTCATCATATGATGAC	120
DB	21	TTPGlyAlaAlaGlyIleLeuLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp	40
QY	121	TATGACCACTTCTTTGAGAGATGTGTACACGCTCATCCCTGTGTAGTATGATCATGTGTA	180

QY 556 CTGGCCACCCCT-----TCCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTA 603
 Db 184 -----TyrProGlnArgAspAlaAspLysValaenGluGluGlyCysPheIleIysVal 201
 QY 604 GTGAAGAAGCTACAAAGAAATCATGATGATGTGATCTGGGCGGCACCTGGCATTTGGAGCT 663
 Db 202 MetThrThrIleGluSerGluMetGlyValValAlaGlyIleSerPheGlyValAlaCys 221
 QY 664 ATTGAGCTGCTGGGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 723
 Db 222 PheGlnLeuIleGlyPheLeuAla---TyrCysLeuSerArgAlaIleThrAsnAsn 240
 QY 724 GCTTACGAGCTCCTC 738
 Db 241 GlnTyrGluIleVal 245

RESULT 5
 S43511
 CD63/ME491 antigen homolog - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 13-Jan-1995 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: S43511
 R:Miyaoto, H.; Homma, M.; Hotta, H.
 Biochim. Biophys. Acta 1217, 312-316, 1994
 A:Title: Molecular cloning of the murine homologue of CD63/ME491 and detection of its s
 A:Reference number: S43511; MUID:94198294; PMID:8148377
 A:Accession: S43511
 A:Molecule type: mRNA
 A:Residues: 1-238 <MI>
 A:Cross-references: UNIPROT:P41731; UNIPARC:UPI00000002B1; EMBL:D16432; NID:9484052; PID
 C:Superfamily: CD9 antigen
 C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
 F:1-11/Domain: intracellular #status predicted <CY1>
 F:12-35/Domain: transmembrane #status predicted <CY1>
 F:36-51/Domain: extracellular #status predicted <EX1>
 F:52-76/Domain: transmembrane #status predicted <CY2>
 F:77-80/Domain: intracellular #status predicted <CY2>
 F:81-103/Domain: transmembrane #status predicted <CY2>
 F:104-202/Domain: extracellular #status predicted <EX2>
 F:203-228/Domain: transmembrane #status predicted <CY3>
 F:229-238/Domain: intracellular #status predicted <CY3>
 F:116,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 5 1e-23 Length: 238
 Score: 330.50 Matches: 79
 Percent Similarity: 53.7% Conservative: 51
 Best Local Similarity: 32.6% Mismatches: 103
 Query Match: 23.1% Indels: 9
 DB: 1 Gaps: 5

US-10-608-388A-1 (1-759) x S43511 (1-238)

QY 13 GGCATCACCTCTCCAGACCGTGTGCTGCTTCTCAACCTCATCTCTCGGGGCGAGCT 72
 Db 6 GlyMetLysCysValLysPheLeuLeuTyrValLeuLeuLeuAlaPheCysAlaCysAla 25
 QY 73 GGCATTTATGCTATGCTGGGAGCCTATGCTTTCATCATCTTATGATGATGATGATGATGAT 132
 Db 26 ValGlyLeuIleAlaIleGlyValAlaValGlnValValLeuLysGlnAlaIleThrHis 45
 QY 133 TTTGAGATGTGTACACCTCATCTGCTGCTAGTATCATAGCTAGTATGAGGCGCTGTT 192
 Db 46 GluThrThrAlaGlySerLeuLeuPro---ValValIleIleAlaValGlyAlaPheLeu 64
 QY 193 TTCATCATGGCTAAATGGTGTGCTGCCCAATCCCGGAAGTCGCTGTGGACTGCC 252
 Db 65 PheLeuValAlaPheValGlyCysCysGlyAlaCysLysGluAsnTyrCysLeuMetile 84
 QY 253 ACGTTTGTATCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 312
 Db 85 ThrPheAlaIlePheLeuSerLeuIleMetLeuValGluValAlaValAlaIleAlaGly 104

QY 313 TATGTTTACAGACAAAGTGGAAATGAGTTGATCGCAGCATTCAGAAAGTGTATAAG 372
 Db 105 TyrValPheArgAspGlnValLysSerGluPheAsnLysSerPheGlnGlnMetGln 124
 QY 373 ACCTACATGGAACCAACCCCTGATGCTGCTAGCCGGCTATTGATTATGTACAGACAG 432
 Db 125 AsnTyrLeuLysAspAsnLysThrAlaThr-----IleLeuAspLysLeuGlnLysGlu 142
 QY 433 CTGCATTGTTGTGAATTCACACTACTCAGACTGGGAAATACAGATTGGTTCAAAGAA 492
 Db 143 AsnAsnCysCysGlyAlaSerAsnTyrThrAspTrpGluAsnIleProGlyMetAlaLys 162
 QY 493 ACCAAACACAGAGTGTCTCTTGTGCTGTGCGAGAGACTGCCCAATTTGTAATGGC 552
 Db 163 AspArg-----ValProAspSerCysCysIleAsnIleThrValGlyCys---Gly 178
 QY 553 AGCTGGCCACCCCTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAAG 612
 Db 179 AsnAspPheLysGluSerThrIleHisThrGlnGlyCysValGluThrIleAlaIleTrp 198
 QY 613 CTCAAGAAATCATGATGATGATGCTGCGGCGCCTGTCATTTGCAGCTATTTCAGCTG 672
 Db 199 LeuArgLysAsnIleLeuValAlaAlaAlaLeuGlyIleAlaPheValGluVal 218
 QY 673 CTGGGACATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
 Db 219 LeuGlyIleIlePheSerCysCysLeuVal-----LysSerIleArgSerGlyTyrGlu 236
 QY 733 CTCCTC 738
 Db 237 ValMet 238

RESULT 6
 A46508
 CD63/ME491 antigen homolog - rat
 N:Alternate names: mast cell antigen AD1
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 18-Jun-1993 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: A46508; S16776
 R:Nishikata, H.; Oliver, C.; Mergenhagen, S.E.; Siraganian, R.P.
 J. Immunol. 149, 862-870, 1992
 A:Title: The rat mast cell antigen AD1 (homologue to human CD63 or melanoma antigen ME:
 A:Reference number: A46508; MUID:92340890; PMID:1634775
 A:Accession: A46508
 A:Molecule type: mRNA
 A:Residues: 1-238 <NTS>
 A:Cross-references: UNIPROT:P28648; UNIPARC:UPI0000167A7D; EMBL:X61654; NID:955601; PII
 A:Note: This antigen was found localized to mast cells in tissue samples, but was induc
 C:Note: sequence extracted from NCBI backbone (NCBI:109346, NCBI:P:109349)
 C:Comment: This heavily glycosylated protein of 50-60K (27K after deglycosylation) is
 C:Superfamily: CD9 antigen
 C:Keywords: glycoprotein; lysosome; mast cell; surface antigen; transmembrane protein
 F:1-11/Domain: intracellular #status predicted <CY1>
 F:12-35/Domain: transmembrane #status predicted <CY1>
 F:36-51/Domain: extracellular #status predicted <EX1>
 F:52-76/Domain: transmembrane #status predicted <CY2>
 F:77-80/Domain: intracellular #status predicted <CY2>
 F:81-103/Domain: transmembrane #status predicted <CY2>
 F:104-202/Domain: extracellular #status predicted <EX2>
 F:203-228/Domain: transmembrane #status predicted <CY3>
 F:229-238/Domain: intracellular #status predicted <CY3>
 F:130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
 Pred. No.: 7.88e-23 Length: 238
 Score: 328.50 Matches: 79
 Percent Similarity: 52.5% Conservative: 48
 Best Local Similarity: 32.6% Mismatches: 106
 Query Match: 23.0% Indels: 9
 DB: 1 Gaps: 5

US-10-608-388A-1 (1-759) x A46508 (1-238)

```

Qy 13 GGCATCACCTCCTCCACAGACCGTGTGCTTTCTCAACCTCATCTTCTGGGGGACGCT 72
Db 13 GGCATCACCTCCTCCACAGACCGTGTGCTTTCTCAACCTCATCTTCTGGGGGACGCT 72
6 GlyMetLysCysValPheLeuLeuTyrValLeuLeuLeuAlaPheCysAlaCysAla 25
Qy 73 GGCATTTTATGCTATGTGGGACCGTATGCTTTCTCACTATGATGATGATGACCATTC 132
Db 73 GGCATTTTATGCTATGTGGGACCGTATGCTTTCTCACTATGATGATGATGACCATTC 132
26 ValGlyLeuLeuAlaAlaValAlaValGlnValLeuLysGlnAlaLeuThrHis 45
Qy 133 TTGAGAGATGTACACGCTCATCCCTGCTGCTGATGATGATGATGATGATGATGATGAT 192
Db 133 TTGAGAGATGTGTACACGCTCATCCCTGCTGCTGATGATGATGATGATGATGATGATGAT 192
46 GluThrThrAlaGlySerLeuLeuPro---ValValIleAlaValAlaValAlaPheLeu 64
Qy 193 TTCTATCATTTGGCTTAATTTGGTGTGCTGCCAATCCGGGAAAGTCTGCTGGACTTGC 252
Db 193 TTCTATCATTTGGCTTAATTTGGTGTGCTGCCAATCCGGGAAAGTCTGCTGGACTTGC 252
65 PheLeuValAlaPheValGlyCysCysGlyAlaCysLysGluAenTyrCysLeuMetIle 84
Qy 253 ACGTTTGTATCATCTGCTCTGTTGTTTGTCTCAGAGAGTGTGTGTGTGTGTGTGTGTGT 312
Db 253 ACGTTTGTATCATCTGCTCTGTTGTTTGTCTCAGAGAGTGTGTGTGTGTGTGTGTGTGT 312
85 ThrPheAlaIlePheLeuSerLeuIleMetLeuValGluValAlaAlaIleAlaGly 104
Qy 313 TATGTTTACAGACCAAGGTGGAATGAGTTCGTCAGCATTCAGAAAGTGTATAAG 372
Db 313 TATGTTTACAGACCAAGGTGGAATGAGTTCGTCAGCATTCAGAAAGTGTATAAG 372
105 TyrValPheArgAspGlnValLysSerGluPheSerLysPheGlnLysGlnMetGin 124
Qy 373 ACCTACCAATGGAACCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Db 373 ACCTACCAATGGAACCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
125 AsnTyrLeuThrAspAsnLysThrAlaThr-----IleLeuAspLysLeuGlnLysGlu 142
Qy 433 CTGATTTGTTGTAATTCACAACTACTCAGACTGGGAAATACAGATTTGTTGTTGTTGTTG 492
Db 433 CTGATTTGTTGTAATTCACAACTACTCAGACTGGGAAATACAGATTTGTTGTTGTTGTTG 492
143 AsnLysCysGlyAlaSerAsnTyrThrAspTrpGluArgIleProGlyMetAlaLys 162
Qy 493 ACCAAAACACAGATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Db 493 ACCAAAACACAGATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
163 AspArg-----ValProAspSerCysCysLeuVal-----LysSerIleArgSerGlyTyrGlu 178
Qy 553 AGCTGTGCTCCACCTCTCCGACCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Db 553 AGCTGTGCTCCACCTCTCCGACCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
179 AsnAspPheLysGluSerThrIleHisThrGlnGlyCysValGluThrIleAlaAlaTrp 198
Qy 613 CTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
Db 613 CTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
199 LeuArgLysAsnValLeuValAlaGlyAlaAlaLeuLeuGlyIleAlaPheValGluVal 218
Qy 673 CTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 673 CTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
219 LeuGlyIleIlePheSerCysCysLeuVal-----LysSerIleArgSerGlyTyrGlu 236
Qy 733 CTCTCTC 738
Db 237 ValMet 238

```

RESULT 7

```

JC2297
CD63 antigen - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 28-Oct-1994 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C:Accession: JC2297
R:Sohma, Y.; Suzuki, T.; Sasano, H.; Nagura, H.; Nose, M.; Yamamoto, T.
Cell Struct. Funct. 19, 219-225, 1994
A:Title: Increased mRNA for CD63 antigen in atherosclerotic lesions of Watanabe heritable
A:Reference number: JC2297; MUID:95120837; PMID:7820873
A:Accession: JC2297
A:Molecule type: mRNA
A:Residues: 1-238 <SOH>
A:Cross-references: UNIPROT:Q28709; UNIPARC:UPI000016C588; DDBJ:D21264; NID:G684973; PII
A:Experimental source: aorta
C:Superfamily: CD9 antigen
C:Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F:11/Domain: intracellular #status predicted <CY1>
F:12-35/Domain: transmembrane #status predicted <TM1>
F:36-51/Domain: extracellular #status predicted <EX1>

```

```

F:52-76/Domain: transmembrane #status predicted <TM2>
F:77-80/Domain: intracellular #status predicted <CY2>
F:81-103/Domain: transmembrane #status predicted <TM3>
F:104-202/Domain: extracellular #status predicted <EX2>
F:203-228/Domain: transmembrane #status predicted <TM4>
F:229-238/Domain: intracellular #status predicted <CY3>
F:125,130,150,172/Binding site: carbohydrate (Asn) (covalent) #status predicted

```

Alignment Scores:

```

Pred. No.: 2,91e-22 Length: 238
Score: 322.50 Matches: 80
Percent Similarity: 51.2% Conservative: 44
Best Local Similarity: 33.1% Mismatches: 109
Query Match: 22.6% Indels: 9
DB: 1 Gaps: 5

```

US-10-608-388A-1 (1-759) x JC2297 (1-238)

```

Qy 13 GGCATCACCTCCTCCACAGACCGTGTGCTTTCTCAACCTCATCTTCTGGGGGACGCT 72
Db 6 GlyMetLysCysValLysPheLeuLeuTyrValLeuLeuLeuAlaPheCysAlaCysAla 25
Qy 73 GGCATTTTATGCTATGTGGGACCGTATGCTTCTCATCCTTATGATGATGATGACCATTC 132
Db 26 ValGlyLeuIleAlaValGlyValAlaGlnValLeuSerGlnThrIleThrHis 45
Qy 133 TTGAGAGATGTGTACACGCTCATCCCTGCTGCTGATGATGATGATGATGATGATGATGAT 192
Db 46 GlyAlaThrProGlySerLeuLeuPro---ValValIleAlaValAlaValAlaPheLeu 64
Qy 193 TTCTATCATTTGGCTTAATTTGGTGTGCTGCCAATCCGGGAAAGTCTGCTGGACTTGC 252
Db 65 PheLeuValAlaPheValGlyCysCysGlyThrCysLysGluAenTyrCysLeuMetIle 84
Qy 253 ACGTTTGTATCATCTGCTCTGTTGTTTGTCTCAGAGAGTGTGTGTGTGTGTGTGTGTGT 312
Db 85 ThrPheAlaIlePheLeuSerLeuIleMetLeuValGluValAlaAlaIleAlaGly 104
Qy 313 TATGTTTACAGACCAAGGTGGAATGAGTTCGTCAGCATTCAGAAAGTGTATAAG 372
Db 105 TyrValPheArgAspLysValMetSerGluPheAsnLysAspPheArgGlnMetGin 124
Qy 373 ACCTACCAATGGAACCAACCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 432
Db 125 AsnTyrSerThrAspAsnGlnThrAlaLeu-----IleLeuAspArgMetGlnLysAsp 142
Qy 433 CTGATTTGTTGTAATTCACAACTACTCAGACTGGGAAATACAGATTTGTTGTTGTTGTTG 492
Db 143 PheThrCysCysGlyAlaAlaAenTyrThrAspTrpAlaThrIleProGlyMetThrArg 162
Qy 493 ACCAAAACACAGATGCTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 552
Db 163 AspArg-----ValProAspSerCysCysValAsnValThrSerGlyCys---Gly 178
Qy 553 AGCTGTGCTCCACCTCTCCGACCTCTATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 612
Db 179 ValLysPheAsnValLysAspIleTyrValGluGlyCysValGluLysIleGlyLeuTrp 198
Qy 613 CTACAGAAATCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 672
Db 199 LeuArgLysAsnValLeuValAlaAlaAlaLeuGlyIleAlaPheValGluVal 218
Qy 673 CTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
Db 219 LeuGlyIleValPheAlaCysCysLeuVal-----LysSerIleArgSerGlyTyrGlu 236
Qy 733 CTCTCTC 738
Db 237 ValMet 238

```

RESULT 8
A59265
tetraspan TSPAN-4 - human

C;Genetics:

A;Gene: GDB:CD63; ML1
A;Cross-references: GDB:I20186; OMIM:155740
A;Map position: 12q13-12q13
A;Introns: 22/3; 85/3; 142/3; 189/3; 217/3
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; lysosome; surface antigen; transmembrane protein
F;2-238/Product: melanoma-associated antigen ME491 #status experimental <NAT>
F;2-11/Domain: intracellular #status predicted <CY1>
F;12-35/Domain: transmembrane #status predicted <EX1>
F;36-51/Domain: extracellular #status predicted <EX1>
F;52-76/Domain: transmembrane #status predicted <TM2>
F;77-80/Domain: intracellular #status predicted <CY2>
F;81-103/Domain: transmembrane #status predicted <TM3>
F;104-202/Domain: extracellular #status predicted <EX3>
F;203-228/Domain: transmembrane #status predicted <TM4>
F;229-238/Domain: intracellular #status predicted <CY3>
F;130,150,172/Binding site: carbohydrate (Asn) #status predicted

Alignment Scores:
Pred. No.: 6.72e-20 Length: 238
Score: 297.50 Matches: 79
Percent Similarity: 50.4% Conservative: 48
Best Local Similarity: 31.3% Mismatches: 96
Query Match: 20.8% Indels: 29
DB: 1 Gaps: 9

US-10-608-388A-1 (1-759) x I38016 (1-238)

QY 13 GGATCATCCTCTCCAGACCGCTGCTCTTCTCAACCTCATCTTCTGGGG---GCA 69
Db 6 GlyMetLysCysValLysPheLeuLeuTyValLeuLeuLeuAlaPheCysAlaCysAla 25
QY 70 GCTGGCATTTATGCTAT---GTGGGAGCTATGCTCTTCATCATCTATGATGACTATGAC 126
Db 26 ValGlyLeuLeuAlaValGlyValGlyAlaGlnLeuValLeuSer----- 40
QY 127 CACTTCTTTGAAGATGTGTACAGCTCATCCTCGCT----- 162
Db 41 -----GlnThrIleGlnGlyAlaThrProGlySerLeuLeuPro 54
QY 163 GTATGATCATAGCTGTAGAGCGCTGCTTTTTCATCATCTGGGTAATGCTGCTGTGCC 222
Db 55 ValValIleIleAlaValGlyValPheLeuPheLeuValAlaPheValGlyCysGly 74
QY 223 ACAATCGGGAAGTGCCTGTGACCTGCCAGCTTGTCTATCATCTGCTCTTGGTTTTT 282
Db 75 AlaCysLysGluAsnTyCysLeuMetIleThrPheAlaIlePheLeuSerLeuIleMet 94
QY 283 GTACAGAACTGTGTGTAGTGGTGTGGATATGTTTACAGACAAAGGTGGAATATGAG 342
Db 95 LeuValGluValAlaAlaAlaIleAlaGlyTyValPheArgAspLysValMetSerGlu 114
QY 343 GTTGATCGACATTCAGAAAGTGTATPAGACCTTACAACTGGAACCACTGTGCTGTCT 402
Db 115 PheAsnAsnAsnPheArgGlnMetGluAsnTyProLysAsnAsnHisThrAlaSer 134
QY 403 AGCGGGCTATTGATATGTATACAGACACAGCTGCATGTTGTGGATTCACACTACTCA 462
Db 135 -----IleLeuAspArgMetGlnAlaAspPheLysCysGlyAlaAlaAsnTyThr 152
QY 463 GACTTGGGAAATACAGATTGTTTCAAGAAACCAACCAAGTGTCCCTCTTAGCTGC 522
Db 153 AspIrpGluLysIlePro-----SerMetSerLysAsnArg---ValProAspSerCys 159
QY 523 TGCAGAGACAGCTGCCAGCAATTTGTAATGGCAGCGCTGGCCCACTTCCGACCTCTATGCT 582
Db 170 CysIleAsnValThrValGlyCys---GlyIleAsnPheAsnGluLysAlaIleHisLys 188
QY 583 GAGGGGTGTAGGCTCTAGTAGTGAAGAACTACAGAAATCATGATGATGATGCTGG 642
Db 189 GluGlyCysValGluLysIleGlyGlyTrpLeuArgLysAsnValLeuValAlaAla 208

QY 643 GCGCACTGGCACTTTGCAGCTATTCAGCTGCTGGCATCTGTGTGCTTCATCGTGTG 702
Db 209 AlaAlaLeuGlyIleAlaPheValGluValLeuGlyIleValPheIaCysCysLeuVal 228
QY 703 TGCAGAAAGAGTAGAGATCTGCTTTAGGAGCTCCTC 738
Db 229 -----LysSerIleArgSerGlyTyGluValMet 238
RESULT 10
A46493
metastasis suppressor KAI1 - human
N;Alternate names: cell surface glycoprotein KAI1; membrane protein R2, inducible; ty
C;Species: Homo sapiens (man)
C;Date: 18-Jun-1993 #sequence revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: I38942; S16156; A46493
R;Dong, J.T.; Lamb, P.W.; Rinker-Schaeffer, C.W.; Vukanovic, J.; Ichikawa, T.; Isaacs, S.
Science 288, 884-886, 1995
A;Title: KAI1, a metastasis suppressor gene for prostate cancer on human chromosome 1:
A;Reference number: I38942; MUID:95273964; PMID:7754374
A;Accession: I38942
A;Status: nucleic acid sequence not shown; translated from GB/EMBL/DBJ
A;Molecule type: mRNA
A;Residues: 1-267 <RES>
A;Cross-references: UNIPROT:P27701; UNIPARC:UPI00001273AE; EMBL:U20770; NID:9806805; I
R;Gautschi, H.W.; Hofer, E.; Huber, N.E.; Schnabl, E.; Baumruker, T.
Eur. J. Immunol. 21, 377-383, 1991
A;Title: A new superfamily of lymphoid and melanoma cell proteins with extensive homo
A;Reference number: S16156; MUID:91153380; PMID:1842498
A;Accession: S16156
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-267 <CAU>
A;Cross-references: UNIPARC:UPI0001273AE; EMBL:X53795; NID:935832; PIDN:CAA37804.1; I
A;Note: the authors translated the codon AGC for residue 50 as Thr
R;Imai, T.; Fukudome, K.; Takagi, S.; Nagira, M.; Furuse, M.; Fukuhara, N.; Nishimura, J.
Immunol. 149, 2879-2886, 1992
A;Title: C33 antigen recognized by monoclonal antibodies inhibitory to human T cell le
D9, CD37, CD53, and CD63.
A;Reference number: A46493; MUID:93017900; PMID:1401919
A;Accession: A46493
A;Status: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-239, 'MV', 242-267 <IMA>
A;Cross-references: UNIPARC:UPI0000163A0; GB:S48196; NID:9258294; PIDN:AAB23825.1; P
A;Experimental source: T-cell line MOLT-4
A;Note: sequence extracted from NCBI backbone (NCBIP:117149)
C;Genetics:
A;Gene: GDB:KAI1
A;Cross-references: GDB:134216; OMIM:600623
A;Map position: 11p11.2-11p11.2
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-57/Domain: extracellular #status predicted <EX1>
F;58-78/Domain: transmembrane #status predicted <TM2>
F;79-83/Domain: intracellular #status predicted <CY2>
F;84-108/Domain: transmembrane #status predicted <TM3>
F;109-227/Domain: extracellular #status predicted <EX2>
F;228-252/Domain: transmembrane #status predicted <TM4>
F;253-265/Domain: intracellular #status predicted <CY3>
F;129,157,198/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:
Pred. No.: 1.57e-18 Length: 267
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservative: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: 1 Gaps: 7

US-10-608-388A-1 (1-759) x A46493 (1-267)

QY	1	ATGGGCCAGTGGCGGATCATCTCTCCAGACCGTGTGGTCTTTCTCAACTCATCTTC	60
Db	1	MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhe	20
QY	61	TGGGGGCGAGCTGGCATTTTATGCTATGTGGGAGCCTATGCTCTCATCACTTATGATGAC	120
Db	21	PheIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAla	37
QY	121	TATGACCACCTTTTGAAGATGTGTACACG	165
Db	38	LysSerSerPheIleSerValIleuGlnThrSerSerSerLeuArgMetGlyAlaTyr	57
QY	166	GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCTTGGCTAATTGGCTGTGTGCCACA	225
Db	58	ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla	77
QY	226	ATCCGGGAAAGTCGCTGTGGACTTCCACGTTTGTTCATCACTCTGCTCTGTTGTTTGTG	285
Db	78	ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuIleLeuIle	97
QY	286	ACAGAAGTGTGTGTAGTGGTTTTGGGATGTATGTTTACAGAGCAAGGCGAAATGAGGTT	345
Db	98	AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet	117
QY	346	GATCGCAGCATTCAGAAAGTGTATAAGACCTACATGGAACCAACCTCATGCTCTCTAGC	405
Db	118	GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln	137
QY	406	CGGCTATTGATTATGATCAGAGACAGCTGCAATGTTGTGGAATTCACAACTACTCAGAC	465
Db	138	AspAlaTrpAspTyrValGlnAlaGlnValLysCysCysGlyTrpValSerPheTyrAsn	157
QY	466	TGGGAAATACAGATTGTTTCAAGAAACCAAAACCAGAGTGTCCCTCTTAGCTGC	522
Db	158	TrpThrAspAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu	177
QY	523	-----TGACAGACGAGACTGCC	537
Db	178	ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys-----GluAlaPro	196
QY	538	AGCAATTGTAATGGCAGCGCTGGCCACCCCTCCGAC-----CTCTATGCTCAGGGGTGT	591
Db	197	GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys	216
QY	592	GAGGCTTAGTAGTGAAGAGCTACAGAAATCATGATGCATGTGATCTGGGCCCGCACTG	651
Db	217	MetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleLeuGlyValGlyVal	236
QY	652	GCATTTGCAGCTATTACGTCGTGGCGCATGCTGTGCTTGCTGCTGTGTGGCAGAAGG	711
Db	237	GlyValAlaIleIleGluLeuLeuGlyMetValLeuSer-----IleCysLeuCysArgHis	255
QY	712	-----AGTAGAGATCCTGCTTAC	729
Db	256	ValHisSerGluAspTyrSerLysValProLysVal	267

RESULT 11

A37243
hemopoietic cell surface glycoprotein CD53 - human
N:Alternate names: pan-leukocyte surface antigen CD53
C:Species: Homo sapiens (man)
C/Date: 30-Dec-1991 #sequence_revision 09-Aug-1996
C/Accession: A37243; A45872
R:Amiot, M.

J. Immunol. 145, 4322-4325, 1990
A>Title: Identification and analysis of cDNA clones encoding CD53. A pan-leukocyte anti-
A;Reference number: A37243; PMID:12258620
A;Accession: A37243
A;Molecule type: mRNA
A;Residues: 1-219 <AMI>
A;Cross-references: UNIPROT:P19397; UNIPARC:UPI000000D991; GB:M60871; NID:P180140; PID:
R:Angelisova, P.; Vlcek, C.; Stefanova, I.; Lipoldova, M.; Horejsi, V.
Immunogenetics 32, 281-285, 1990

A,Title: The human leucocyte surface antigen CD53 is a protein structurally similar to
A,Reference number: A45872; MUID:91055810; PMID:1700763
A,Accession: A45872
A,Molecule type: mRNA
A,Residues: 1-219 <ANG>
A,Cross-references: UNIPARC:UPI000000D991; GB:M37033; NID:g180142; PIDN:AAA35663.1; PII:
C,Genetics:
A,Gene: GDB:CD53; MOX44
A,Cross-references: GDB:127521; OMIM:151525
A,Map position: lp21-lp13.3
C,Superfamily: CD5 antigen
C,Keywords: glycoprotein; transmembrane protein
F,1-10/Domain: intracellular #status predicted <CY1>
F,11-36/Domain: transmembrane #status predicted <TM1>
F,37-54/Domain: extracellular #status predicted <EX1>
F,55-75/Domain: transmembrane #status predicted <TM2>
F,76-80/Domain: intracellular #status predicted <CY2>
F,81-106/Domain: transmembrane #status predicted <TM3>
F,107-181/Domain: extracellular #status predicted <EX2>
F,182-204/Domain: transmembrane #status predicted <TM4>
F,205-219/Domain: intracellular #status predicted <CY3>
F,1-29,148/Binding site: carbohydrate (Asn) (covalent) #status predicted

Alignment Scores:

Alignment Scores:			
Pred. No.:	1,25e-17	Length:	219
Score:	273.50	Matches:	65
Percent Similarity:	46.2%	Conservative:	44
Best Local Similarity:	27.5%	Mismatches:	100
Query Match:	19.1%	Indels:	27
DB:	1	Gaps:	4

US-10-608-388A-1 (1-759) x A37243 (1-219)

Qy	1	ATGGGCAGTGCGGCATCACTCTCTCAAGACCGTGCTGTGCTTTCTCAACTCATCTATCTTC	60
Db	1	MetGlyMetSerSerLeuLeuLysLeuValLeuPhePheAsnLeuLeuPhe	20
Qy	61	TGGGGGCGAGCTGGCATTTATGCTATGTGGAGCGCTATGCTTCATCATCTCACTTTATCATGAC	120
Db	21	TrpIleCysGlyCysCysIleLeuGlyPheGlyIleIleIleLeuLeuIle--HisAsnAsn	39
Qy	121	TATGACCACCTCTTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATCATCTAGCTGTA	180
Db	40	PheGlyValLeuPheHisAsnLeuProSerLeuThrLeuGlyAsnValPheValIleVal	59
Qy	181	GGAGCCCTGCTTTTCATCATTTGGCGCTAATTGGCTGCTGTGCCACAAATCGGGAAGATCCG	240
Db	60	GlySerIleIleMetValAlaPheLeuGlyCysMetGlySerIleLysGluAsnLys	79
Qy	241	TGTGGACTTCCACGTTGTGTCATCATCTCTGCTCTTGGTTTTTGTGCACAGAAGTCTGTGTA	300
Db	80	CysLeuLeuMetSerPheIleLeuLeuLeuIleIleLeuLeuAlaGluValThrLeu	99
Qy	301	GTGCTTTTGGCATATGTTTACAGACGAAAGGTGGAAAATGAGTGTGATCGCAGCATCTACAG	360
Db	100	AlaIleLeuLeuPheValTyrGluGlnLysLeuAsnGluTyrValAlaLysGlyLeuThr	119
Qy	361	AAAGTGTAAGACCTCAATAGGAACCAACCTGATGCTGTAGCGGGGCTATTGATAT	420
Db	120	AspSerIleHisArgTyrHisSerAspAsnSerThrLysAla-----AlaTrpAspSer	137
Qy	421	GTACAGAGACAGCTGCATTGTTGGGAATTCACAACTACTCAGACTGGGAAAATACAGAT	480
Db	138	IleGlnSerPheLeuGlnCysCysGlyIleAsnGlyThrSerAspTrp-----	153
Qy	481	TGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTAGCTGTGCAGAGAGACTGCCAGC	540
Db	154	-----ThrSerGlyProIleAsnSerCys-----	161
Qy	541	AATTGTAATGGCAGCGCTGGGCCACCTTCGACCTCTATGTGTAGGGGTGTGAGGCTCTA	600
Db	162	-----ProSerAspArgLysValGluGlyCysTyrAlaLys	173

QY 601 GTAGTGAAGAAGCTACAGAATAATCATGATGATGATGCTGGCGGCACTGGCATTTGCA 660
Db 174 AlaArgLeuTrpPheHisSerAsnPheLeuTyrileGlyIleIleThrIleCysValCys 193
QY 661 GCTATTACGCTGGGGCATGCTGTGCTTGGCATCGGTGGTGGAG 708
Db 194 ValIleGluValLeuGlyMetSerPheAlaLeuThrLeuAsnCysGln 209
RESULT 12
A59262
tetraspan TSPAN-1 - human
C;Species: Homo sapiens (man)
C;Date: 19-May-2000 #sequence_revision 19-May-2000 #text_change 09-Jul-2004
C;Accession: A59262
R;Todd, S.C.; Doctor, V.S.; Levy, S.
Biochim. Biophys. Acta 1399, 101-104, 1998
A;Title: Sequences and expression of six new members of the tetraspanin/TM4SF family.
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-241 <TOD>
A;Cross-references: UNIPROT:O60635; UNIPARC:UPI000004BE36; GB:AF054838; NID:g2997740; PII
C;Genetics:
C;Superfamily: CD9 antigen
Alignment Scores:
Pred. No.: 1.23e-16 Length: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
Gaps: 2
US-10-608-388a-1 (1-759) x A59262 (1-241)
QY 7 CAGTGGCGGCATCCTCTCCAGACGCTGCTGCTTCTTCACTCATCTTCTGGGG 66
Db 2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuIlePheLeu 20
QY 67 GCAGCTGGCATTTTATGCTATGCTGGAGCCTATGCTTCTCATCTTATGATGACTATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
QY 127 CACTTCTTGAAGATGCTACACGCTCATCCTCTGCTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGAGCCCTGCTTTTTCATCATTTGGGCTAATTTGGCTGCTGCTGCCACATCCGG 231
Db 61 IleAlaAlaGlyValValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
QY 232 GAAAGTCGCTGTGACTTGGCAGCTTTGTCTATCATCTGCTTGTGTTTTGTGCACAGAA 291
Db 81 GluSerLysCysAlaLeuValThrPhePheIleLeuLeuIlePheIleAlaGlu 100
QY 292 GTTGTGTAGTGGTTTGGGATATGTTTACAGACCAAGGTGGAAATAGGTTGATCGC 351
Db 101 ValAlaAlaAlaValValAlaLeuValTyrThrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 AGCATTCAGAAAGTGATATACACCTACAAATGGACCAACCTCATGCTGCTAGCCGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluAsp----PheThrGlnVal 139
QY 412 ATTGATTATACAGACAGCTGCATTGTTGTGGAAATTCACAACTACTCAGACTGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATACAGATTGGTTTCAAGAAACCAAAACACAGAGTCTCCTCTTACTGCTGCTGAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177

QY 532 ACTGCCAGCAAT-----TGTATATGGCAGCTGGCCCACTTCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrGluGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATCATGTG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
QY 637 ATCTGGGCGCACTGGCATTTGCGAGCTATTACGCTGCTGGCAGCTGTGCTTGTGATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTGTGTGTC 705
Db 236 LeuTyrCys 238
RESULT 13
A39574
leukocyte antigen OX-44 - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 30-Aug-1991 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
C;Accession: A39574
R;Bellacosa, A.; Izzo, P.A.; Bear, S.E.; Tsichlis, P.N.
Mol. Cell. Biol. 11, 2864-2872, 1991
A;Title: The rat leukocyte antigen MRC OX-44 is a member of a new family of cell surf.
A;Reference number: A39574; MUID:91203909; PMID:2017181
A;Accession: A39574
A;Molecule type: mRNA
A;Residues: 1-219 <BEL>
A;Cross-references: UNIPROT:P24485; UNIPARC:UPI000004F1F0; GB:M57276; NID:g205897; PII
C;Superfamily: CD9 antigen
C;Keywords: glycoprotein; transmembrane protein
F;1-10/Domain: intracellular #status predicted <CY1>
F;11-36/Domain: transmembrane #status predicted <TM1>
F;37-54/Domain: extracellular #status predicted <EX1>
F;55-73/Domain: transmembrane #status predicted <CY2>
F;74-79/Domain: intracellular #status predicted <CY2>
F;80-106/Domain: transmembrane #status predicted <TM3>
F;107-181/Domain: extracellular #status predicted <EX2>
F;182-204/Domain: transmembrane #status predicted <TM4>
F;205-219/Domain: intracellular #status predicted <CY3>
F;119,129,148/Binding site: carbohydrate (Asn) (covalent) #status predicted
Alignment Scores:
Pred. No.: 2.64e-16 Length: 219
Score: 259.50 Matches: 61
Percent Similarity: 45.3% Conservative: 46
Best Local Similarity: 25.8% Mismatches: 102
Query Match: 18.2% Indels: 27
Gaps: 4
US-10-608-388a-1 (1-759) x A39574 (1-219)
QY 1 ATGGGCGCAGTGGGCATCACCTCTCCAGACGCTGCTGCTTTCTTCAACCTCATCTTC 60
Db 1 MetGlyMetSerSerLeuLysLeuLeuLysTyrValLeuPhePheAsnPheLeuPhe 20
QY 61 TGGGGGCGAGCTGGCATTTTATGCTATGCTGGGCGCTATGCTTCTCATCATTATGATGAC 120
Db 21 TrpValCysGlyCysCysIleLeuGlyPheGlyIleHisLeuLeuVal---GlnAsnThr 39
QY 121 TATGACCACTTCTTTCAAGATGTGTACACGCTCATCCCTGCTGTAGTGATCATGCTGTA 180
Db 40 TyrGlyIleLeuPheArgAsnLeuPropheLeuThrLeuGlyAsnValLeuValIleVal 59
QY 181 GGAGCCCTCTTTTCATCATTTGGGCTAATTTGGCTGCTGTGCCACAATCCGGGAAGTCGC 240
Db 60 GlySerIleIleMetValValAlaPheLeuGlyCysMetGlySerIleLysGluAsnLys 79
QY 1241 TGTGGACTTGGCCAGCTTTTGTCTATCCTCTGCTCTTGGTTTGTTCACAGAAGTTGTGTA 300
Db 80 CysLeuLeuMetSerPhePheValLeuLeuLeuIleLeuLeuAlaGluValThrLeu 99

QY 301 GTGGTTTGGGATATGTTTACAGACAAAGGTGGAAATAGAGTTGATCGCAGCATTCAG 360
 Db
 QY 100 AlalleLeuLeuPheValTyrGluLysIleAsnThrLeuValAlaGluGlyLeuAsn 119
 Db
 QY 361 AAAGTGTATAACACATACAAAGAACCAACCTGATGCTGCTAGCGGGCTATTGATTAT 420
 Db
 QY 120 AspSerIleGlnHisTyrHisSerAspAsn-----SerThrArgMetAlaTrpAspPhe 137
 Db
 QY 421 GTACAGACAGCTGCATTTGTTGGAATTCACAACTACTCAGACTGGGAATACAGAT 480
 Db
 QY 138 IleGlnSerGlnLeuGlnCysGlyValAlaAsnGlySerSerAspTrp----- 153
 Db
 QY 481 TGGTTCAAAGAAACCAAAACCCAGAGTGTCCCTCTTACCTGTCTGTCAGAGACTGCCAGC 540
 Db
 QY 154 -----IleSerGlyProProSerSerCys----- 161
 Db
 QY 541 AATTGTAATGCGAGCTGCCACCCCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
 Db
 QY 162 -----ProSerGlyAlaAspValGlnGlyCysTyrLysLys 173
 Db
 QY 601 GTAGTGAAAGACTACAAAGAATCATGATGATGATGCTGGCGCCACTGGCATTGCA 660
 Db
 QY 174 GlyGlnAlaTrpPheHisSerAsnPheLeuTyrIleGlyIleValThrIleCysValCys 193
 Db
 QY 661 GCTATTACGCTGCGGATGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 708
 Db
 QY 194 ValIleGlnValLeuGlyMetSerPheAlaLeuThrLeuAsnCysGln 209
 Db
 RESULT 14
 I49561
 C33/R2/IA4 - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
 C:Accession: I49561
 R:Nagira, M.; Imai, T.; Ishikawa, I.; Uwabe, K.I.; Yoshie, O.
 Cell: Immunol. 157, 144-157, 1994
 A:Title: Mouse homologue of C33 antigen (CD82), a member of the transmembrane 4 superfamily
 A:Reference number: I49561; MUID:94313678; PMID:8039242
 A:Accession: I49561
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-266 <RES>
 A:Cross-references: UNIPROT:P40237; UNIPARC:UPI0000022B1C; GB:D14883; NID:9984036; PIDN:
 C:Superfamily: CD9 antigen
 Alignment Scores:
 Pred. No.: 2,626-16 Length: 266
 Score: 259.50 Matches: 76
 Percent Similarity: 43.6% Conservative: 43
 Best Local Similarity: 27.8% Mismatches: 117
 Query Match: 18.2% Indels: 37
 DB: 2 Gaps: 9
 US-10-608-388A-1 (1-759) x I49561 (1-266)
 QY 1 ATGGGCGAGTGGGATGCTTCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
 Db
 QY 1 MetGlyAlaGlyCysValLysValThrLysTyrPheLeuPheLeuPheAsnLeuPhe 20
 Db
 QY 61 TGGGGCGGAGCTGGCATTTTATGCTATGCTGGGAGCTATGCTTCATCATCTTATGATGAC 120
 Db
 QY 21 PheIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAla-----Asp 37
 Db
 QY 121 TATGACCACTCTTTGAAGATGTGTACAG-----CTCATCCCTGCTGCTA 165
 Db
 QY 38 LysAsnSerPheIleSerValLeuGlnThrSerSerSerSerLeuGlnValGlyAlaTyr 57
 Db
 QY 166 GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCATTTGGCTAAATGGCTGTGGCCACA 225
 Db
 QY 58 ValPheIleGlyValGlyAlaIleThrIleValMetGlyPheLeuGlyCysIleGlyAla 77
 Db
 QY 226 ATCCGGGAAGTCGCTGTGGACTTCCAGCTTTGTTCATCATCTGCTCTGCTGTTTGTG 285
 Db

Db 78 ValAsnGluValArgCysLeuLeuLeuGlyLeuTyrPheValPheLeuLeuLeuLeuLeu 97
 QY 286 ACAGAGTTGTTGTTAGTGGTGGTATATGTTTACAGACAAAGGTGGAAATAGAGTTT 345
 Db
 QY 98 AlaGlnValThrValGlyValLeuPheTyrPheAsnAlaAspLysLeuLysGluMet 117
 Db
 QY 346 GATCGCAGCATTCAGAAAGTGTATAAGCACTCAATGGAACCAACCTGATGCTGCTAGC 405
 Db
 QY 118 GlyAsnThrValMetAspIleIleArgAsnTyrThrAlaAsnAlaThrSerSerArgGlu 137
 QY 406 CGGCTATTGATTATGACAGACAGCTGCATTTGTTGGAATTCACAACTACTCATCAGAC 465
 Db
 QY 138 GluAlaTrpAspTyrValGlnAlaGlnValLysCysGlyTrpValSerHisTyrAsn 157
 QY 466 TGG---CAAAATACAGATTGGTTCAAGAAACCAAAACCCAGAGTGTCCCTCTTAGCTGC 522
 Db
 QY 158 TrpThrGluAsnGluGluLeuMetGlyPheThrLysThr---ThrTyrProCysSerCys 176
 QY 523 -----TGCAGAGAGACT 534
 Db
 QY 177 GluLysIleLysGluGluAspAsnGlnLeuIleValLysLysGlyPheCysGlu----- 194
 QY 535 GCCAGCAATTTGTAATGGCAGCCCTGGCCACCTTCCGAC-----CTCATGCTGAGGGG 588
 Db
 QY 195 AlaAspAsnSerThrValSerGluAsnAsnProGluAspTrpProValAsnThrGluGly 214
 QY 589 TGTGAGCTCTAGTAGTAAGAGCTACAAGAATCATGATGCTGATGCTGGGCCGCA 648
 Db
 QY 215 CysMetGluLysAlaGlnAlaTrpLeuGlnGluAsnPheGlyIleLeuLeuGlyValCys 234
 QY 649 CTGGCATTTGCGAGCTATTGAGCTGCTGGGCGATGCTGTGCTGCTGCTGCTGCTGCTG 708
 Db
 QY 235 AlaGlyValAlaValIleGluLeuLeuGlyLeuPheLeuSer---IleCysLeuCysArg 253
 QY 709 -----AGGAGTAGAGATCTGCTTAC 729
 Db 254 TyrIleHisSerGluAspTyrSerLysValProLysTyr 266
 RESULT 15
 B47629
 cell surface glycoprotein CD37 - rat
 N:Alternate names: leukocyte antigen CD37
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 03-Feb-1994 #sequence_revision 09-Aug-1996 #text_change 09-Jul-2004
 C:Accession: B47629; JCI501
 R:Classon, B.J.; Williams, A.F.; Willis, A.C.; Seed, B.; Stamenkovic, I.
 J. Exp. Med. 172, 1007, 1990
 A:Reference number: A47629; MUID:90354767; PMID:2388030
 A:Accession: B47629
 A:Molecule type: mRNA
 A:Residues: 1-281 <CLA>
 A:Cross-references: UNIPROT:P31053; UNIPARC:UPI0000127351; EMBL:X53517; NID:955911; PII
 C:Comment: This antigen is expressed abundantly on B lymphocytes and is also seen at l
 C:Superfamily: CD9 antigen
 C:Keywords: glycoprotein; lymphocyte; transmembrane protein
 F:2-12/Domain: intracellular #status predicted <CY1>
 F:13-38/Domain: transmembrane #status predicted <TM1>
 F:39-59/Domain: extracellular #status predicted <EX1>
 F:60-80/Domain: transmembrane #status predicted <TM2>
 F:81-85/Domain: intracellular #status predicted <CY2>
 F:86-110/Domain: transmembrane #status predicted <TM3>
 F:111-241/Domain: extracellular #status predicted <EX2>
 F:242-267/Domain: transmembrane #status predicted <TM4>
 F:268-278/Domain: intracellular #status predicted <CY3>
 F:170,183,188/Binding site: carbohydrate (Asn) (covalent) #status predicted
 Alignment Scores:
 Pred. No.: 4,05e-16 Length: 281
 Score: 257.50 Matches: 71
 Percent Similarity: 43.2% Conservative: 46
 Best Local Similarity: 26.2% Mismatches: 115
 Query Match: 18.0% Indels: 39
 DB: 1 Gaps: 8

GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:34:40 ; Search time 11.3 Seconds
(without alignments)
1819.174 Million cell updates/sec

Title: US-10-608-388A-1
Perfect score: 1429
Sequence: 1 atggggccagcggccatcac.....tcaactggcggaacctatgca 759

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Fgapop 10.0 , Fgapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 572472 seqs, 135419439 residues

Total number of hits satisfying chosen parameters: 1144944

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+n2p.model -DEV=xlp
-Q=/abes/ABSWEB_spoel/US10608388/runat_04042006_150701_14229/app_query.fasta_1
-DB=Pending Patents AA New -QFMT=fastan -SUFFIX=n2p.rapn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100
-MAXLEN=2000000000 -HOST=abes02p
-USER=US10608388 @CGN 1.1_97 @runat_04042006_150701_14229 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBL=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6 -Fgapext=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Pending Patents AA New.*
1: /SID55/ptodata/2/paa/PCT NEW COMB.pcp.*
2: /SID55/ptodata/2/paa/US06 NEW COMB.pcp.*
3: /SID55/ptodata/2/paa/US07 NEW COMB.pcp.*
4: /SID55/ptodata/2/paa/US08 NEW COMB.pcp.*
5: /SID55/ptodata/2/paa/US09 NEW COMB.pcp.*
6: /SID55/ptodata/2/paa/US10 NEW COMB.pcp.*
7: /SID55/ptodata/2/paa/US11 NEW COMB.pcp.*
8: /SID55/ptodata/2/paa/US60 NEW COMB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1336	93.5	253	6	US-10-917-503B-11371
2	1336	93.5	253	6	Sequence 11371, A
3	1329	93.0	253	6	US-10-917-503B-11412
4	1329	93.0	253	6	Sequence 11412, A
5	343.5	24.0	244	6	US-10-917-503B-11363
6	343.5	24.0	244	6	Sequence 11363, A
7	332	23.2	253	6	US-10-529-348-2235
8	332	23.2	253	6	Sequence 2235, Ap
9	332	23.2	253	6	US-11-268-554-266
10	332	23.2	253	6	Sequence 266, App
11	332	23.2	253	6	US-11-268-554-267
12	332	23.2	253	6	Sequence 267, App
13	332	23.2	253	6	US-11-268-554-269
14	332	23.2	253	6	Sequence 269, App
15	332	23.2	253	6	US-11-268-554-272
16	332	23.2	253	6	Sequence 272, App
17	332	23.2	253	6	US-10-567-867-1300
18	332	23.2	253	6	Sequence 1300, Ap

10	332	23.2	253	7	US-11-385-692-2034	Sequence 2034, Ap
11	332	23.2	253	7	US-11-385-692-2035	Sequence 2035, Ap
12	332	23.2	253	7	US-11-385-692-2037	Sequence 2037, Ap
13	332	23.2	253	7	US-11-385-692-2040	Sequence 2040, Ap
14	331	23.2	253	6	US-11-268-554-273	Sequence 273, App
15	331	23.2	253	6	US-10-567-867-1298	Sequence 1298, App
16	331	23.2	253	7	US-11-385-692-2041	Sequence 2041, Ap
17	316.5	22.1	254	1	PCT-US05-40623-8	Sequence 8, Appli
18	316.5	22.1	254	6	US-11-270-040-8	Sequence 8, Appli
19	304	21.3	211	6	US-11-268-554-268	Sequence 268, App
20	304	21.3	211	7	US-11-385-692-2036	Sequence 2036, Ap
21	303	21.2	259	6	US-10-276-817B-9769	Sequence 9769, Ap
22	301.5	21.1	238	1	PCT-US06-02704-28	Sequence 28, Appl
23	301.5	21.1	238	6	US-11-339-733-28	Sequence 28, Appl
24	297.5	20.8	237	8	US-60-741-048-215	Sequence 215, App
25	297.5	20.8	238	6	US-11-332-890-2	Sequence 2, Appli
26	297.5	20.8	238	8	US-60-741-048-216	Sequence 216, App
27	297.5	20.8	238	8	US-60-741-048-217	Sequence 217, App
28	297.5	20.8	238	8	US-60-741-048-218	Sequence 218, App
29	297.5	20.8	238	8	US-60-741-048-219	Sequence 219, App
30	283	19.8	267	6	US-10-276-817B-12889	Sequence 12889, A
31	283	19.8	267	8	US-60-763-374-1	Sequence 1, Appli
32	282.5	19.8	239	6	US-10-917-503B-13815	Sequence 13815, A
33	282.5	19.8	239	6	US-10-567-867-1603	Sequence 1603, Ap
34	282.5	19.8	239	8	US-60-751-420-2526	Sequence 2526, Ap
35	282	19.7	267	8	US-60-763-374-3	Sequence 3, Appli
36	282	19.7	267	8	US-60-763-374-4	Sequence 4, Appli
37	282	19.7	331	8	US-60-763-374-2	Sequence 2, Appli
38	273.5	19.1	219	5	US-09-836-544D-36	Sequence 36, Appl
39	263	18.4	241	6	US-11-191-274A-76	Sequence 76, Appl
40	263	18.4	241	6	US-11-191-274A-77	Sequence 77, Appl
41	263	18.4	241	6	US-11-191-274A-78	Sequence 78, Appl
42	263	18.4	241	6	US-11-191-274A-79	Sequence 79, Appl
43	263	18.4	241	6	US-11-191-274A-80	Sequence 80, Appl
44	263	18.4	241	6	US-11-191-274A-81	Sequence 81, Appl
45	263	18.4	241	6	US-11-344-932-114	Sequence 114, App

ALIGNMENTS

RESULT 1
US-10-917-503B-11371
; Sequence 11371, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OFA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORI
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH CDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18

```
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11371
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11371

Alignment Scores:
Pred. No.: 5,83e-123 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 6 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-917-503B-11371 (1-253)

Qy 1 ATGGCCAGTGGGCATCACCTCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

Qy 61 TGGGGCGAGCTGGCATTATGCTATGTGGAGCTATGCTTTCATCACTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyraasp 40

Qy 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCCCTGCTAGTGTATGATCTGA 180
Db 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValIleAlaVal 60

Qy 181 GGAGCCCTGCTTTTCATCATCTGCTCTGCTGCACACATCGGGAAGTCCG 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80

Qy 241 TGTGACTTGCACGTTTGTTCATCATCTGCTCTTGGTTTGTGTCACAGAAGTTCGA 300
Db 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100

Qy 301 GTGGTTTGGGATATGTTTACAGACAAAGTGGAAATGAGTGTGATCGGAGCTTACG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120

Qy 361 AAGTGTATAGACCTACATGAGACCAACCTGATGCTGTAGCGGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140

Qy 421 GTACAGACAGCTGCATTGTTGTGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160

Qy 481 TGGTTCAAAGAAACCAAAACACAGAGTGTCCCTCTTATGCTGTGACAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180

Qy 541 AATTGTATAGGAGCTGGCCACCTCCGACCTCTATGCTAGCGGGTGTGAGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200

Qy 601 GTAGTGAAGAGCTACAAGAATCATGATGATGATGCTGGCCGCGACTGTCATTTGCA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220

Qy 661 GCTATTTCAGCTGCTGGGATGCTGTGTGCTGTCATCGTGTGTGTGTCAGAGGAGTAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240

Qy 721 CCTGCTTACGAGCTCTCATCACTCGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyraAla 253

RESULT 2
```

```
US-10-917-503B-11412
; Sequence 11412, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; CURRENT FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/09/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 11412
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11412

Alignment Scores:
Pred. No.: 5,83e-123 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 6 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-917-503B-11412 (1-253)

Qy 1 ATGGCCAGTGGGCATCACCTCTCCAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerLysThrValLeuValPheLeuAsnLeuIlePhe 20

Qy 61 TGGGGCGAGCTGGCATTATGCTATGTGGAGCTATGCTTTCATCACTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyraasp 40

Qy 121 TATGACCACTCTTTGAAGATGTGTACACGCTCATCCCTGCTAGTGTATGATCTGA 180
Db 41 TyrAspHisPhePheGluaspValTyrThrLeuIleProAlaValIleAlaVal 60

Qy 181 GGAGCCCTGCTTTTCATCATCTGCTCTGCTGCACACATCGGGAAGTCCG 240
Db 61 GlyAlaLeuLeuPheIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80

Qy 241 TGTGACTTGCACGTTTGTTCATCATCTGCTCTTGGTTTGTGTCACAGAAGTTCGA 300
Db 81 CysGlyLeuAlaThrPheValIleLeuLeuValPheValThrGluValValVal 100

Qy 301 GTGGTTTGGGATATGTTTACAGACAAAGTGGAAATGAGTGTGATCGGAGCTTACG 360
```

```
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAGACCTCAATAGGAACCAACCTGATGCTGCTAGCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaLaserArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCATTGTTGTGAATTACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTTPGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACCAAGAGTGTCCCTTTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAAGAAATCATGATGTCATCTGGCGGCAGCTGGCATTTCGA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaPheAla 220
Qy 661 GCTATTACGCTGGCGCAGCTGCTGTGCTTGTGATCGTGTGTCAGAGAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 3

```
US-10-917-503B-11363
; Sequence 11363, Application US/10917503B
; GENERAL INFORMATION:
; APPLICANT: OTA, TOSHIO
; APPLICANT: ISOGAI, TAKAO
; APPLICANT: NISHIKAWA, TETSUO
; APPLICANT: HAYASHI, KOJI
; APPLICANT: SAITO, KAORU
; APPLICANT: YAMAMOTO, JUNICHI
; APPLICANT: ISHII, SHIZUKO
; APPLICANT: SUGIYAMA, TOMOYASU
; APPLICANT: WAKAMATSU, AI
; APPLICANT: NAGAI, KEIICHI
; APPLICANT: OTSUKI, TETSUJI
; TITLE OF INVENTION: PRIMERS FOR SYNTHESIZING FULL-LENGTH cDNA AND THEIR USE
; FILE REFERENCE: 084335/0123
; CURRENT APPLICATION NUMBER: US/10/917,503B
; PRIOR FILING DATE: 2004-08-13
; PRIOR APPLICATION NUMBER: US/05/629,469
; PRIOR FILING DATE: 2000-07-28
; PRIOR APPLICATION NUMBER: JP 1999-248036
; PRIOR FILING DATE: 1999-07-29
; PRIOR APPLICATION NUMBER: JP 1999-300253
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: JP 2000-118776
; PRIOR FILING DATE: 2000-01-11
; PRIOR APPLICATION NUMBER: JP 2000-183767
; PRIOR FILING DATE: 2000-05-02
; PRIOR APPLICATION NUMBER: JP 2000-241899
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/159,590
; PRIOR FILING DATE: 1999-10-18
; PRIOR APPLICATION NUMBER: 60/183,322
; PRIOR FILING DATE: 2000-02-17
; NUMBER OF SEQ ID NOS: 19025
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11363
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-917-503B-11363
```

Alignment Scores:

```
Pred. No.: 2,85e-122 Length: 253
Score: 1329.00 Matches: 252
Percent Similarity: 99.6% Conservatives: 0
Best Local Similarity: 99.6% Mismatches: 1
Query Match: 93.0% Indels: 0
DB: 6 Gaps: 0
```

US-10-608-388A-1 (1-759) x US-10-917-503B-11363 (1-253)

```
Qy 1 ATGGGCGAGTGGCGCATCACCTCTCCAAAGACCGTGTGCTTTCTCAACCTCATCTTC 60
Db 1 MetGlyGlnCysGlyIleThrSerSerLysThrValLeuValPheLeuAsnLeuIlePhe 20
Qy 61 TGGGGGCGCAGCTGGCATTTTATGCTATGTGGGAGCCTATGCTCTCATCTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyIleLeuCysTyrValGlyAlaTyrValPheIleThrTyrAspAsp 40
Qy 121 TATGACCACTCTTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTGATCATAGCTGTA 180
Db 41 TyrAspHisPhePheGluAspValTyrThrLeuIleProAlaValValIleIleAlaVal 60
Qy 181 GGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTGCCACAATCCGGGAAAGTCGC 240
Db 61 GlyAlaLeuLeuPheIleIleGlyLeuIleGlyCysCysAlaThrIleArgGluSerArg 80
Qy 241 TGTGGACTTGGCCACGTTTGTCTCATCTCTGCTCTGTTTGTCTCAGAGAGTGTGTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleIleLeuLeuLeuValPheValThrGluValAlaVal 100
Qy 301 GTGGTTTTGGGATATGTTTACAGAGCAAAAGGTGGAATGAGTGTGATCCGAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
Qy 361 AAAGTGTATAGACCTCAATAGGAACCAACCTGATGCTGTGCTAGCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
Qy 421 GTACAGACAGCTGCATTGTTGTGAATTCACAACTACTCAGACTGGGAAATACAGAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTTPGluAsnThrAsp 160
Qy 481 TGGTTCAAGAAACCAAAACCAAGAGTGTCCCTTTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTATGCTGAGGGGTGTGAGGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
Qy 601 GTAGTGAAGAGCTACAAAGAAATCATGATGTCATGCTGAGGGGTGTGAGGCTCTA 660
Db 201 ValValLysLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaPheAla 220
Qy 661 GCTATTACGCTGGCGCAGCTGCTGTGCTTGTGATCGTGTGTCAGAGAGAGTAGAGAT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysGlyArgSerArgAsp 240
Qy 721 CCTGCTTACGAGCTCCTCATCACTGGCGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuIleThrGlyGlyThrTyrAla 253
```

RESULT 4

```
US-10-529-348-2235
; Sequence 2235, Application US/10529348
; GENERAL INFORMATION:
; APPLICANT: Bodary-Winter, Sarah
; APPLICANT: Clark, Hilary
; APPLICANT: Jackman, Janet
; APPLICANT: Schoenfeld, Jill
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
```


Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValValAla 190
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyGlyCysIle 209
Qy 595 GCTCTAGTAGTGAAGAAGCTACAGAAATCATGATGTCATGTGCTGGCCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
Qy 655 TTTCGAGCTATTACAGTCTGCTGGCATGCTGTGTCTTC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242
RESULT 8
US-11-268-554-272
; Sequence 272, Application US/11268554
; GENERAL INFORMATION:
; APPLICANT: DOMON, Bruno et al.
; TITLE OF INVENTION: PANCREATIC CANCER TARGETS AND USES
; TITLE OF INVENTION: THEREOF
; FILE REFERENCE: CLO01557
; CURRENT APPLICATION NUMBER: US/11/268,554
; CURRENT FILING DATE: 2005-11-08
; NUMBER OF SEQ ID NOS: 1004
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 272
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-268-554-272
Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: Gaps: 4
US-10-608-388A-1 (1-759) x US-11-268-554-272 (1-253)
Qy 10 TGCGGCATCACCTCTCCAGACCGTCTGTGTTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
Qy 70 GCTGCGATTTTATGCTATGTGGAGCCTATGCTTCATCATCACTATGATGACTATGACCA 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
Qy 130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATGATCATAGTGTAGGACCC 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
Qy 190 CTTTTCATCATTTGGCTAAATGGCTGTGTCACAAATCCGGGAAGTCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
Qy 250 GCCAGCTTTGTCATCTCTCTGTTTGTTCACAGAGTTGTTGTAGTGTGTTTGT 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleAlaGlyIleLeu 110
Qy 310 GGATATGTTTACAGAGCAAGTGGAAATGAGTTGATCGCAGATTTCAG---AAAGTG 366
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130
Qy 367 TATAGACTCAATAGGAACCAACCTGATGCTGTAGCCGGCTATTGATTATATACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
Qy 427 AGACAGCTGCATTGTTGTGGAATTCACAACTACTCAGACTGTGGAAATACAGATTGTTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170

Qy 487 AAA-----GAACCAAAACCAGAGTGTCCTTCTAGCTGCTGCAGAGAGACTGCCAGC 540
Db 171 ArgSerGlnGluAlaGlyGlyArgValValProAspSerCysCysLysThrValValAla 190
Qy 541 AATTGTAATGGCAGCTGGCCACCTTCCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyGlyCysIle 209
Qy 595 GCTCTAGTAGTGAAGAAGCTACAGAAATCATGATGTCATGTGCTGGCCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
Qy 655 TTTCGAGCTATTACAGTCTGCTGGCATGCTGTGTCTTC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242
RESULT 9
US-10-567-867-1300
; Sequence 1300, Application US/10567867
; GENERAL INFORMATION:
; APPLICANT: Li, Martha
; APPLICANT: Rupnow, Brent A.
; APPLICANT: Webster, Kevin R.
; APPLICANT: Jackson, Donald
; APPLICANT: Wong, Tai W.
; TITLE OF INVENTION: BIOMARKERS OF CYCLIN-DEPENDENT KINASE MODULATION
; FILE REFERENCE: D0310 PCT
; CURRENT APPLICATION NUMBER: US/10/567,867
; CURRENT FILING DATE: 2006-01-27
; PRIOR APPLICATION NUMBER: US 60/490,890
; PRIOR FILING DATE: 2003-07-29
; NUMBER OF SEQ ID NOS: 2786
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 1300
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-567-867-1300
Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: Gaps: 4
US-10-608-388A-1 (1-759) x US-10-567-867-1300 (1-253)
Qy 10 TGCGGCATCACCTCTCCAGACCGTCTGTGTTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
Qy 70 GCTGCGATTTTATGCTATGTGGAGCCTATGCTTCATCATCACTATGATGACTATGACCA 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
Qy 130 TTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTGTATGATCATAGTGTAGGACCC 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
Qy 190 CTTTTCATCATTTGGCTAAATGGCTGTGTCACAAATCCGGGAAGTCGCTGTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgAsnLeuLeu 90
Qy 250 GCCAGCTTTGTCATCTCTCTGTTTGTTCACAGAGTTGTTGTAGTGTGTTTGT 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleAlaGlyIleLeu 110
Qy 310 GGATATGTTTACAGAGCAAGTGGAAATGAGTTGATCGCAGATTTCAG---AAAGTG 366
Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAsnThrGluLeuLysGluAsnLeuLysAspThrMet 130


```

QY 367 TATAAGACCTACAAATGGAACCAACCTGCTGCTAGCGGGCTATTGATTGTACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
QY 427 AGACAGCTGCTATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY 487 AAA-----GAAACCAAAACCAAGAGTGCCTCTTACGCTGCTGCAGAGACTGCCAGC 540
Db 171 ArgSerGlnGluAlaGlyArgValValProAspSerCysCysLysThrValValAla 190
QY 541 AATTGTAATGCGACCTGGCCACCCTTCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyCysIle 209
QY 595 GCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGCGCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTTCAGCTATTACGCTGGGCGATGCTGTGCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 10
US-11-385-692-2034
; Sequence 2034, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2034
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2034

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

US-10-608-388A-1 (1-759) x US-11-385-692-2034 (1-253)
QY 10 TGGGGCATCACCTCCTCCAAAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
QY 70 GCTGGCATTTTATGCTATGCTGGAGCCTATGCTTCATCATCTATGATGATGATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
QY 130 TTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTATGATCATGCTGTAGGAGCCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
QY 190 CTTTTCATCATTTGGCTAAATGGCTGTGCTGCCACAAATCGGAAAGTCCGCTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
QY 250 GCCAGCTTTGCTATCATCTGCTCTTGGTTTGTGCACAGAGTGTGTGTAGTGGTTTG 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleIleAlaGlyIleLeu 110
QY 310 GGATATGTTTACAGCAAGGTGGAAATAGAGTTGATGCTGACGATTCAG---AAGTG 366

```

```

Db 111 AlaTyrAlaTyrTyrGlnGlnLeuAenThrGluLeuLysGluAenLeuLysAspThrMet 130
QY 367 TATAAGACCTACAAATGGAACCAACCTGCTGCTAGCGGGCTATTGATTGTACAG 426
Db 131 ThrLysArgTyrHisGlnProGlyHisGluAlaValThrSerAlaValAspGlnLeuGln 150
QY 427 AGACAGCTGCTATTGTTGGAAATTCACAACTACTCAGACTGGGAAATACAGATTGGTTC 486
Db 151 GlnGluPheHisCysCysGlySerAsnAsnSerGlnAspTrpArgAspSerGluTrpIle 170
QY 487 AAA-----GAAACCAAAACCAAGAGTGCCTCTTACGCTGCTGCAGAGACTGCCAGC 540
Db 171 ArgSerGlnGluAlaGlyArgValValProAspSerCysCysLysThrValValAla 190
QY 541 AATTGTAATGCGACCTGGCCACCCTTCGACCTCTAT-----GCTGAGGGGTGTGAG 594
Db 191 LeuCys---GlyGlnArgAspHisAlaSerAsnIleTyrLysValGluGlyCysIle 209
QY 595 GCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATGATGCTGGCGCGCACTGGCA 654
Db 210 ThrLysLeuGluThrPheIleGlnGluHisLeuArgValIleGlyAlaValGlyIleGly 229
QY 655 TTTCAGCTATTACGCTGGGCGATGCTGTGCTTGC 693
Db 230 IleAlaCysValGlnValPheGlyMetIlePheThrCys 242

RESULT 11
US-11-385-692-2035
; Sequence 2035, Application US/11385692
; GENERAL INFORMATION:
; APPLICANT: JOSELOFF, Elizabeth et al.
; TITLE OF INVENTION: KIDNEY DISEASE TARGETS AND USES THEREOF
; FILE REFERENCE: CL0015910RD
; CURRENT APPLICATION NUMBER: US/11/385,692
; CURRENT FILING DATE: 2006-03-22
; NUMBER OF SEQ ID NOS: 6044
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2035
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-385-692-2035

Alignment Scores:
Pred. No.: 4,21e-24 Length: 253
Score: 332.00 Matches: 67
Percent Similarity: 51.1% Conservative: 52
Best Local Similarity: 28.8% Mismatches: 108
Query Match: 23.2% Indels: 6
DB: 7 Gaps: 4

US-10-608-388A-1 (1-759) x US-11-385-692-2035 (1-253)
QY 10 TGGGGCATCACCTCCTCCAAAGACCGTGTGCTCTTCTCAACCTCATCTTCTGGGGGCA 69
Db 11 CysGlyThrValCysLeuLysTyrLeuLeuPheThrTyrAsnCysCysPheTrpLeuAla 30
QY 70 GCTGGCATTTTATGCTATGCTGGAGCCTATGCTTCATCATCTATGATGATGATGACCAC 129
Db 31 GlyLeuAlaValMetAlaValGlyIleTrpThrLeuAlaLeuLysSerAspTyrIleSer 50
QY 130 TTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTATGATCATGCTGTAGGAGCCTG 189
Db 51 LeuLeuAlaSerGlyThrTyrLeuAlaThrAlaTyrIleLeuValValAlaGlyThrVal 70
QY 190 CTTTTCATCATTTGGCTAAATGGCTGTGCTGCCACAAATCGGAAAGTCCGCTGGACTT 249
Db 71 ValMetValThrGlyValLeuGlyCysCysAlaThrPheLysGluArgArgAsnLeuLeu 90
QY 250 GCCAGCTTTGCTATCATCTGCTCTTGGTTTGTGCACAGAGTGTGTGTAGTGGTTTG 309
Db 91 ArgLeuTyrPheIleLeuLeuIlePheLeuLeuGluIleIleAlaGlyIleLeu 110

```


GenCore version 5.1.7
Copyright (c) 1993 - 2006 Bioceleration Ltd.

OM nucleic - protein search, using frame_plus_n2p model

Run on: April 4, 2006, 21:50:24 ; Search time 3.5 Seconds
(without alignments)
1320.309 Million cell updates/sec

Title: US-10-608-388A-1

Perfect score: 1429

Sequence: 1 atggcgccagcgccgcatcac.....tcactggcggaacctatgca 759

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 180808 seqs, 30441898 residues

Total number of hits satisfying chosen parameters: 361616

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

-MODEL=frame+ n2p.model -DEV=xlp
-Q=/abss/ABSSWEB_spool/US10608388/runat_04042006_150709_14367/app_query.fasta_1
-DB=Published Applications_AA_New -QFMT=fastan -SUFFIX=n2p.rapbn -MINMATCH=0.1
-LOOPCL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DICALIGN=200 -THR SCORE=pct -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=ptc -NORM=ext -HEAPSIZ=500 -MINLEN=0
-MAXLEN=2000000000 -HOST=abs02p
-USER=US10608388@cgn_1_1_24 @runat_04042006_150709_14367 -NCPU=6 -ICPU=3
-NO MMAP -NEG SCORES=0 -WAIT -DSPBLOC=100 -LONGLOG -DEV TIMEOUT=120
-WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6 -FGAPEXT=7
-YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

Published Applications_AA_New.*
1: /SID55/ptodata/2/pubpaa/US08_NEW_PUB.pcp.*
2: /SID55/ptodata/2/pubpaa/US06_NEW_PUB.pcp.*
3: /SID55/ptodata/2/pubpaa/US07_NEW_PUB.pcp.*
4: /SID55/ptodata/2/pubpaa/PCT_NEW_PUB.pcp.*
5: /SID55/ptodata/2/pubpaa/US05_NEW_PUB.pcp.*
6: /SID55/ptodata/2/pubpaa/US10_NEW_PUB.pcp.*
7: /SID55/ptodata/2/pubpaa/US11_NEW_PUB.pcp.*
8: /SID55/ptodata/2/pubpaa/US60_NEW_PUB.pcp.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result #No.	Score	Query Match	Length	ID	Description
1	1336	93.5	253	6	US-10-501-035-248
2	453	31.7	222	7	US-11-019-711-81
3	283	19.8	267	6	US-10-627-952-20
4	283	19.8	327	6	US-10-821-234-1686
5	282	19.7	267	6	US-10-329-258-25
6	263	18.4	241	6	US-10-745-586-35
7	263	18.4	241	7	US-11-019-711-77
8	263	18.4	241	7	US-11-019-711-78
9	263	18.4	241	7	US-11-234-786-114

10	251	17.6	237	7	US-11-108-172-1062	Sequence 1062, Ap
11	251	17.6	243	7	US-11-108-172-1122	Sequence 1122, Ap
12	251	17.6	446	7	US-11-108-172-1121	Sequence 1121, Ap
13	250.5	17.5	282	7	US-11-019-711-80	Sequence 80, Appl
14	234.5	16.4	344	7	US-11-108-172-1085	Sequence 1085, Ap
15	228	16.0	240	7	US-11-019-711-76	Sequence 76, Appl
16	226.5	15.9	247	7	US-11-019-711-79	Sequence 79, Appl
17	218.5	15.3	227	7	US-11-029-188-6	Sequence 6, Appl
18	218.5	15.3	228	6	US-10-821-234-1266	Sequence 1266, Ap
19	217	15.2	241	7	US-11-019-711-22	Sequence 22, Appl
20	196	13.7	270	6	US-10-453-372-462	Sequence 462, App
21	196	13.7	270	6	US-10-453-372-464	Sequence 464, App
22	184	12.9	305	6	US-10-063-703-108	Sequence 108, App
23	184	12.9	305	7	US-11-102-240-108	Sequence 108, App
24	184	12.9	305	7	US-11-103-195-108	Sequence 108, App
25	165.5	11.6	126	5	US-09-978-360A-555	Sequence 555, App
26	146.5	10.3	204	7	US-11-080-991-8	Sequence 8, Appl
27	146.5	10.3	204	7	US-10-517-696-108	Sequence 108, App
28	128.5	9.0	80	6	US-10-475-075-860	Sequence 860, App
29	110.5	7.7	196	6	US-10-644-807-293	Sequence 293, App
30	107.5	7.5	273	7	US-11-096-568A-22023	Sequence 22023, A
31	107.5	7.5	273	7	US-11-096-568A-26249	Sequence 26249, A
32	107.5	7.5	316	7	US-11-096-568A-22022	Sequence 22022, A
33	107.5	7.5	317	7	US-11-096-568A-26248	Sequence 26248, A
34	98	6.9	282	7	US-11-096-568A-23450	Sequence 23450, A
35	97	6.8	220	7	US-11-096-568A-23451	Sequence 23451, A
36	95.5	6.7	204	7	US-11-096-568A-23452	Sequence 23452, A
37	93.5	6.5	1113	7	US-11-067-811-4	Sequence 4, Appl
38	92	6.4	954	6	US-10-453-372-1150	Sequence 1150, Ap
39	92	6.4	1268	6	US-10-453-372-1144	Sequence 1144, Ap
40	92	6.4	1268	6	US-10-453-372-1154	Sequence 1154, Ap
41	92	6.4	1288	6	US-10-453-372-1146	Sequence 1146, Ap
42	92	6.4	1288	6	US-10-453-372-1152	Sequence 1152, Ap
43	92	6.4	1408	6	US-10-453-372-1148	Sequence 1148, Ap
44	89	6.2	565	6	US-10-055-877-228	Sequence 228, App
45	87.5	6.1	510	7	US-11-096-568A-34036	Sequence 34036, A

ALIGNMENTS

RESULT 1
US-10-501-035-248
; Sequence 248, Application US/10501035
; Publication No. US20060046249A1
; GENERAL INFORMATION:
; APPLICANT: Bristol-Myers Squibb Company
; TITLE OF INVENTION: IDENTIFICATION OF POLYNUCLEOTIDES AND POLYPEPTIDE FOR PREDICTII
; TITLE OF INVENTION: ACTIVITY OF COMPOUNDS THAT INTERACT WITH PROTEIN TYROSINE KIN
; FILE REFERENCE: D0185 PCT
; CURRENT APPLICATION NUMBER: US/10/501,035
; CURRENT FILING DATE: 2004-07-09
; PRIOR APPLICATION NUMBER: US 60/350,061
; PRIOR FILING DATE: 2002-01-18
; NUMBER OF SEQ ID NOS: 795
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 248
; LENGTH: 253
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-501-035-248

Alignment Scores:
Pred. No.: 3 24e-120 Length: 253
Score: 1336.00 Matches: 253
Percent Similarity: 100.0% Conservative: 0
Best Local Similarity: 100.0% Mismatches: 0
Query Match: 93.5% Indels: 0
DB: 6 Gaps: 0

US-10-608-388A-1 (1-759) x US-10-501-035-248 (1-253)

QY 1 ATGGCGCCAGTGGCGCATCACCTCTCCAGACCGTGCTGCTTTTCTCAACCTCATCTTC 60

Db 1 MetGlyGlnCysGlyLeuThrSerSerLysThrValLeuValPheLeuAsnLeuLeuPhe 20
QY 61 TGGGGGGCAGCTGGCATTATGCTATGTTGGAGGCTATGCTTTCATCATCTTATGATGAC 120
Db 21 TrpGlyAlaAlaGlyLeuLeuGlyCysValGlyAlaValPheLeuThrTrpAspAsp 40
QY 121 TATGACCACTTTTGAAGATGTACAGCTGCATCCCTGCTGTAGTGTATGATCATCTGTA 180
Db 41 TyrAspHisPheGluAspValTyrThrLeuLeuProAlaValValLeuLeuAlaVal 60
QY 181 GGAGCCCTCTTTTCATCATCTGGCTAAATGGCTGTGCTGCACACATCCGGGAAAGTGGC 240
Db 61 GlyAlaLeuLeuPheLeuLeuGlyLeuLeuGlyCysCysAlaThrIleArgGluSerArg 80
QY 241 TGTGCACTTGGCAGCTTCTCATCATCTGCTGCTTGGTGTGTTTGTGCAGAAATGTTGTA 300
Db 81 CysGlyLeuAlaThrPheValIleLeuLeuLeuValPheValThrGluValValVal 100
QY 301 GTGGTTTGGGATGTTTACAGACCAAGGTGGAAATGAGTTTCAGCGCAGCATTCAG 360
Db 101 ValValLeuGlyTyrValTyrArgAlaLysValGluAsnGluValAspArgSerIleGln 120
QY 361 AAAGTGTATAAGACCTTACAACTGGAATTCACAACTCTAGCTGCTAGCGGCTATTGATTAT 420
Db 121 LysValTyrLysThrTyrAsnGlyThrAsnProAspAlaAlaSerArgAlaIleAspTyr 140
QY 421 GTACAGACAGCTGCTATGTTGTGAATTCACAACTCTAGCTGCTAGCGGCTATTGATTAT 480
Db 141 ValGlnArgGlnLeuHisCysCysGlyIleHisAsnTyrSerAspTrpGluAsnThrAsp 160
QY 481 TGGTTCAAGAAACCAAAACAGAGTGCTCTTCTAGCTGTGCTGCTGCTGCTGCTGCTGCT 540
Db 161 TrpPheLysGluThrLysAsnGlnSerValProLeuSerCysCysArgGluThrAlaSer 180
QY 541 AATTGTAATGAGCCTGCGCCACCTCTCCGACCTCTATGCTGAGGGGTGCTGAGCTCTA 600
Db 181 AsnCysAsnGlySerLeuAlaHisProSerAspLeuTyrAlaGluGlyCysGluAlaLeu 200
QY 601 GTAGTGAAGAGCTACAAGAAATCATGATGCTATGCTGCTGCTGCTGCTGCTGCTGCTGCT 660
Db 201 ValValLysLeuGlnGluIleMetMetHisValIleTrpAlaAlaLeuAlaPheAla 220
QY 661 GCTATTACGCTGCTGGCAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 720
Db 221 AlaIleGlnLeuLeuGlyMetLeuCysAlaCysIleValLeuCysArgArgSerArgAsp 240
QY 721 CTGCTTACGAGCTCTCTCATCTACTGCGGGAACCTATGCA 759
Db 241 ProAlaTyrGluLeuLeuLeuLeuThrGlyGlyThrTyrAla 253

RESULT 2

US-11-019-711-81
; Sequence 81, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malvankar, Uriel M
; APPLICANT: Rothenberg, Mark

Alignment Scores: 1.31e-35 Length: 222
Pred. No.: 453.00 Matches: 86
Score: 59.7% Conservative: 49
Best Local Similarity: 38.1% Mismatches: 85
Query Match: 31.7% Indels: 6
Gaps: 3

US-10-608-388A-1 (1-759) x US-11-019-711-81 (1-222)
QY 28 AAGACCGTGTGCTCTTCTCAACTCATCTCTCTGGGGGCGAGCTGGCATTTTATGCTAT 87
Db 1 LysTyrLeuLeuPheLeuLeuAsnLeuLeuPheTrpLeuCysGlyIleLeuLeuAla 20
QY 88 GTGGGAGCCTATGCTTTCATCATCTTATGATGATGATGATGATGATGATGATGATGATGAT 147
Db 21 ValGlyIleTrpLeuLeuValAspLeuSerPheSerGluLeuLeuGlySerLeuSer 40
QY 148 AGCTCATCTGCTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGTGTAGT 207
Db 41 SerLeuValAlaAlaTyrValLeuIleAlaValGlyAlaIleLeuPheLeuValGlyPhe 60
QY 208 ATTGGCTGTGCTGCACCAATCCGGAAAGTCCGCTGTGCTGCTGCTGCTGCTGCTGCTGCT 267
Db 61 LeuGlyCysCysGlyAlaIleArgGluSerArgCysLeuLeuGlyLeuTyrPheValPhe 80
QY 268 CTGCTCTTGGT 327
Db 81 LeuLeuLeuIlePheIleLeuGluValAlaAlaGlyIleLeuAlaPheValPheArgAsp 100

QY 328 AAGTGGAAATGAGTTGATCGGAGCATTGAGAAAGTGATATAGACCTCAATGGAC 387
DB 101 LysLeuGluSerSerLeuAsnGluSerLeuLysAsnAlaLeuLysAsnTyrTrpAspThr 120
QY 388 AACCTGATGCTGCTAGCGGGCTATTGATTATGTACAGACAGAGCTGCTATTGTGGA 447
DB 121 AspProAspGluArgAsn--AlaTrpAspLysLeuGluGlnPheLysCysGly 139
QY 448 ATTCACAACTACTAGCTGGGAAATACAGATTGTTTCAAGAAACCAAAACACAGAGT 507
DB 140 ValAsnGlyTyrThrAspTrpPheAspSerGlnTrpPhe-----SerAsnGly 155
QY 508 GTCCCTCTTACGTGCTGACAGAGAGCTGCCAGCAATTGTAATGCGAGCTGGCCACCT 567
DB 156 ValProPheSerCysCysAsnProSerValSer---CysAsnSerAlaGlnAspGlu 174
QY 568 TCCGACCTTATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATG 627
DB 175 AspThrIleTyrGlnGlyCysLeuGluLysLeuLeuGluTrpLeuGluGluAsnLeu 194
QY 628 ATGATGATGCTGGCGGCACTGGCATTTCAGCTATTTCAGCTGCTGGGCACTGCTGT 687
DB 195 LeuIleValGlyGlyValAlaLeuGlyLeuAlaLeuIleGlnLeuLeuGlyMetIleLeu 214
QY 688 GCTTGCATCGTGTGTGC 705
DB 215 SerCysLeuCysCys 220

RESULT 3
US-10-627-952-20
; Sequence 20, Application US/10627952
; Publication No. US20050250102A1
; GENERAL INFORMATION:
; APPLICANT: Dong, Jin-Tang; Barrett,
; J. Carl; Lamb, Patricia W.; Isaacs, John T.
; TITLE OF INVENTION: DIAGNOSTIC METHODS AND
; GENE THERAPY USING REAGENTS DERIVED FROM THE
; HUMAN METASTASIS SUPPRESSOR GENE KAI1
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORGAN & FINNEGAN, L.L.P.
; STREET: 345 PARK AVENUE
; CITY: NEW YORK
; STATE: NEW YORK
; COUNTRY: USA
; ZIP: 10154
; COMPUTER READABLE FORM:
; MEDIUM TYPE: FLOPPY DISK
; COMPUTER: IBM PC COMPATIBLE
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: MICROSOFT WORD 97
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/627,952
; FILING DATE: 24-Jul-2003
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/795,380
; FILING DATE: 27-Feb-2001
; APPLICATION NUMBER: 09/232,507
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: RICHARD W. BORK
; REGISTRATION NUMBER: 36,459
; REFERENCE/DOCKET NUMBER: 2026-4172US1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 758-4800
; TELEFAX: (212) 751-6849
; TELEX: 421792
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 267 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown

TOPOLOGY: unknown
SEQUENCE DESCRIPTION: SEQ ID NO: 20:
US-10-627-952-20

Alignment Scores:
Pred. No.: 2,59e-19 Length: 267
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservatives: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: 6 Gaps: 7

US-10-608-388A-1 (1-759) x US-10-627-952-20 (1-267)

QY 1 ATGGGCGAGTGGCGGATCACCTCTCAAGACCGTGTGTCTTCTCAACCTCATCTTC 60
DB 1 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheLeuLeuPhe 20
QY 61 TGGGGGGCAGCTGGCATTATGCTATGTGGGAGCCCTATCTTCTCATCTTATGATGAC 120
DB 21 PheIleLeuGlyAlaValIleLeuGlyPheGlyValTrpIleLeuAla-----Asp 37
QY 121 TATGACCACTTCTTCAAGATGTGTACAG-----CTCATCCCTGTGTGTA 165
DB 38 LysSerSerPheIleSerValLeuGlnThrSerSerSerLeuArgMetGlyAlaTyr 57
QY 166 GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCATTTGGGCTAATTGGCTGTGTCACA 225
DB 58 ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla 77
QY 226 ATCCGGGAAAGTGGCTGTGGACCTGTGCACGTTTGTTCATCATCTGCTTGTGTTTGTG 285
DB 78 ValAsnGluValArgCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuLeuLeu 97
QY 286 ACAGAAAGTTGTGTAGTGGTGTGGATATGTTTACAGACAAAGGTGGAATAGAGTT 345
DB 98 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 117
QY 346 GATCGCAGCATTCAGAAAGTGTATAGACCTACAAATGGAAACCAACCTGTGTGTGCTAGC 405
DB 118 GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 137
QY 406 CGGGCTATTGATTATGTACAGACAGCTGCTGCTTTGTTGGAATTCACAACTACTCAGAC 465
DB 138 AspAlaTrpAspTyrValGlnAlaGlnValLysCysGlyTrpValSerPheTyrAsn 157
QY 466 TGGGAAATACAGATTGGTTCAAGAAACCAAAACACAGAGTGTCCCTCTTGTAGCTGC--- 522
DB 158 TrpThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu 177
QY 523 -----TGCAGAGAGACTGCC 537
DB 178 ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro 196
QY 538 AGCAATTGTAATGGCAGCTGGCCACCTTCCGAC-----CTCTATGCTGAGGGGTGT 591
DB 197 GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys 216
QY 592 GAGGCTCTAGTAGTGAAGAGCTACAGAAATCATCATGATGATGTGCGGCGGCACTG 651
DB 217 MetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleLeuGlyValGlyVal 236
QY 652 GCATTGCGAGCTATTTCAGCTGCTGGGCACTGCTGTGTGCTGTGCTGTGTGTCAGAGG 711
DB 237 GlyValAlaIleIleGluLeuLeuGlyMetValLeuSer---IleCysLeuCysArgHis 255
QY 712 -----AGTAGAGATCCTGCTTAC 729
DB 256 ValHisSerGluAspTyrSerLysValProLysTyr 267

RESULT 4
US-10-821-234-1686
; Sequence 1686, Application US/10821234

```
; Publication No. US20050255114A1
; GENERAL INFORMATION:
; APPLICANT: Labat, Ivan
; APPLICANT: Stache-Crain, Birgit
; APPLICANT: Andarmani, Susan
; APPLICANT: Tang, Y. Tom
; TITLE OF INVENTION: Methods for Diagnosis and Treatment of Presclampsia
; FILE REFERENCE: 821A
; CURRENT APPLICATION NUMBER: US/10/821,234
; CURRENT FILING DATE: 2004-04-07
; PRIOR APPLICATION NUMBER: US 60/462,047
; PRIOR FILING DATE: 2003-04-07
; NUMBER OF SEQ ID NOS: 1704
; SOFTWARE: pt_seq_genes Version 1.0
; SEQ ID NO 1686
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-821-234-1686

Alignment Scores:
Pred. No.: 2,63e-19 Length: 327
Score: 283.00 Matches: 78
Percent Similarity: 43.8% Conservative: 41
Best Local Similarity: 28.7% Mismatches: 119
Query Match: 19.8% Indels: 34
DB: 6 Gaps: 7

US-10-608-388A-1 (1-759) x US-10-821-234-1686 (1-327)
QY 1 ATGGGGCAGTGGGACCTCTTCAAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 61 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhe 80
QY 61 TGGGGGGCAGCTGGCATATTTATGCTATGATGGGAGCGCTATGCTTCACTCATCTATGATGAC 120
Db 81 PheIleLeuGlyAlaValIleLeuGlyPheGlyValThrIleLeuAla-----Asp 97
QY 121 TATGACCATTCTTTCAAGATGTGTACACG-----CTCATCCCTGCTGTA 165
Db 98 LysSerSerPheIleSerValLeuGlnThrSerSerSerSerSerSerSerLeuArgMetGlyAlaTyr 117
QY 166 GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCATCTGGGCTAATGGCTGTGCTGCCACA 225
Db 118 ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla 137
QY 226 ATCCGGGAAAGTCGCTGGGACTTGGCCACGTTTGTGCATCATCTCTCTGTTGTTTGTTC 285
Db 158 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 177
QY 346 GATCGAGCATTCAAGAAAGTGTATAGCTTCAAGAACCAACCAACCTGATCTGCTAGC 405
Db 178 GlyGlyIleValThrCluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 197
QY 406 CGGGCTATTGATATGATACAGACAGCTGTCATTTGTGGTAATTCACAATCTACAGAC 465
Db 198 AspAlaTrpAspTyrValGlnAlaGlnValLysCysCysGlyTrpValSerPheTyrAsn 217
QY 466 TGGGAAATACAGATTGGTTTCAAGAAACCAACCAACCAAGAGTGTCCCTTGTAGTGC--- 522
Db 218 TrpThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu 237
QY 523 -----TGACAGAGACTGCC 537
Db 238 ValLysGlyGluGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro 256
QY 538 AGCAATTGTAATGGACCTGGGCCACCTCTCCGAC-----CTCTATCTCAGGGGTGT 591
Db 257 GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys 276
```

```
; Publication No. US20060024233A1
; GENERAL INFORMATION:
; APPLICANT: MUELLER, SABINE
; APPLICANT: GONZALEZ-ZULUETA, MIRELLA
; APPLICANT: FORHR, ERIK
; APPLICANT: CHIN, DANIEL J.
; TITLE OF INVENTION: USE OF BIOMOLECULAR TARGETS IN THE TREATMENT AND VISUALIZATION (
; FILE REFERENCE: AGYT-008US2
; CURRENT APPLICATION NUMBER: US/10/329,258
; CURRENT FILING DATE: 2002-12-23
; PRIOR APPLICATION NUMBER: 60/343,422
; PRIOR FILING DATE: 2001-12-27
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patent in version 3.1
; SEQ ID NO 25
; LENGTH: 267
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-329-258-25

Alignment Scores:
Pred. No.: 3,23e-19 Length: 267
Score: 282.00 Matches: 77
Percent Similarity: 43.8% Conservative: 42
Best Local Similarity: 28.3% Mismatches: 119
Query Match: 19.7% Indels: 34
DB: 6 Gaps: 7

US-10-608-388A-1 (1-759) x US-10-329-258-25 (1-267)
QY 1 ATGGGCAGTGGGACCTCTCTCAAGACCGTGGTCTTCTCAACCTCATCTTC 60
Db 1 MetGlySerAlaCysIleLysValThrLysTyrPheLeuPheLeuPheAsnLeuIlePhe 20
QY 61 TGGGGGGCAGCTGGCATTTTATGCTATGATGGGAGCGCTATGCTTCTCATCTATGATGAC 120
Db 21 PheIleLeuGlyAlaValIleLeuGlyPheGlyValThrIleLeuAla-----Asp 37
QY 121 TATGACCATTCTTTGAAGATGTGTACACG-----CTCATCCCTGCTGTA 165
Db 38 LysSerSerPheIleSerValLeuGlnThrSerSerSerSerSerSerSerLeuArgMetGlyAlaTyr 57
QY 166 GTGATCATAGCTGTAGGAGCCCTGCTTTTCATCATCTGGGCTAATGGCTGTGCTGCCACA 225
Db 58 ValPheIleGlyValGlyAlaValThrMetLeuMetGlyPheLeuGlyCysIleGlyAla 77
QY 226 ATCCGGGAAAGTCGCTGGGACTTGGCCACGTTTGTGCATCATCTCTCTGTTGTTTGTTC 285
Db 78 ValAsnGluValAlaGlyCysLeuLeuGlyLeuTyrPheAlaPheLeuLeuLeuIleLeuIle 97
QY 286 ACAGAAAGTGTGTAGTGGTTTGGGATATGTTTACAGACAAAGGTGGAAATGAGTT 345
Db 98 AlaGlnValThrAlaGlyAlaLeuPheTyrPheAsnMetGlyLysLeuLysGlnGluMet 117
QY 346 GATCGAGCATTCAAGAAAGTGTATAGCTTCAAGAACCAACCAACCTGATCTGCTAGC 405
Db 118 GlyGlyIleValThrGluLeuIleArgAspTyrAsnSerSerArgGluAspSerLeuGln 137
```


Qy		406	CGGGCTATTGATTTGTACAGAGACAGCTGCATTTGTTGGAAATTCACAACACTACTCAGAC	465
Dd		138	AspAlatTrpAspTyrValGlnAlaGlnValLysCysGlyTrpValSerPheTyrAsn	157
Qy		466	TGGGAATAACAGATTGGTTCAAGAANAACCAAACCAGAGTGTCCTCTTAGCTGC---	522
Dd		158	ThrThrAspAsnAlaGluLeuMetAsnArgProGluValThrTyrProCysSerCysGlu	177
Qy		523	-----TGCAGAGACAGACTGCC	537
Dd		178	ValllysGlyGluAspAsnSerLeuSerValArgLysGlyPheCys---GluAlaPro	196
Qy		538	AGCAATTCTAATGGCAGCTGGCCCAACCTTCCGAC-----CTCATGCTCAGGGGTCT	591
Dd		197	GlyAsnArgThrGlnSerGlyAsnHisProGluAspTrpProValTyrGlnGluGlyCys	216
Qy		592	GAGGCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATGCATGTCATGTGGGCCCGCACTG	651
Dd		217	MetGluLysValGlnAlaTrpLeuGlnGluAsnLeuGlyIleIleucGlyValGlyVal	236
Qy		652	GCATTGTGACGCTATTCAGCTGCTGGGCATGCTGTGTGCTTGCATCGTGTGTGCAGAAGG	711
Dd		237	GlyValAlaIleValGluLeuLeuGlyMetValLeuSer---IleCysLeuCysArgHis	255
Qy		712	-----AGTAGAGATCCTGCTTAC	729
Dd		256	ValHisSerGluAspTyrSerLysValProLysTyr	267

Qy 67 GCAGCTGGCAATTTATGTAATGTTGGGAGCCATATGCTCTCATCACTTATGATGACTATGAC 120
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
Qy 127 CACTTCTTTGAAGATGTGTACACGCTCATCCCTGCTGTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
Qy 172 ATAGCTTAGGAGCCCTGCTTTTCATCATTTGGGTAAATGTGCTGCTGCCACAAATCCGG 231
Db 61 IleAlaAlaGlyValValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
Qy 232 GAAAGTCGCTGTGACACTGGCCACGTTGTTCATCATCTCTGCTCTGTTGTTTGTACAGNA 291
Db 81 GluSerLysCysAlaLeuValThrPhePhePheIleLeuLeuLeuPheIleAlaGlu 100
Qy 292 GTTGTCTAGTGTGTTTGGGATATGTTTACAGAGCAAAAGGTGGAAAATGAGGTTGATCGC 351
Db 101 ValAlaAlaValValAlaLeuValTyrThrThrMetAlaGluHisPheLeuThrLeu 120
Qy 352 AGCATTCAGAAAGTGTATAGACCTACAAATGGAACCAACCTGTATGTCTAGCGGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluAsp---PheThrGlnVal 139
Qy 412 ATTGATTTATGTACAGACAGCTGCATTTGTTGGAATTCACAACTACTCAGACTGGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
Qy 472 AATACATGTTGTTTCAAGAAACCAAAACCAGAGTGTCCCTCTTACGCTGTGCAGAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177
Qy 532 ACTGCCCAAGCAAT-----TGTAATGGCAGCCTGGCCCACTTCCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrLysGlnLysAlaHis-----AspGln 195
Qy 577 TATGCTGAGGGGTGTGAGGCTTAGTAGTGAAGAGCTACAAGAAATCATGATGATGTG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
Qy 637 ATCTGGGGCCACTGGCATTTTGCAGCTATTACAGCTGTGGGCGCATGCTGTGCTTGCATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
Qy 697 GTGTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 7
US-11-019-711-77
; Sequence 77, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia

```

; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 77
; LENGTH: 241
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-019-711-77

Alignment Scores:
Pred. No.: 2,128-17 Length: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
DB: 7 Gaps: 6

US-10-608-388a-1 (1-759) x US-11-019-711-77 (1-241)
QY 7 CAGTGGCGCATCACCTCTCCAGACCGTGTGCTTTCTCAACCTCATCTCTTGGGGG 66
Db 2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuIlePheLeu 20
QY 67 GCAGCTGGCATTATTTATGTATGGAGCCTATGCTTCATCATCTATGACTATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleLysPheIleAspGlyAlaSerPheLeu 40
QY 127 CACTCTTTTGAGATGTGTACAGCTCATCCCTGCTGTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGGAGCCTGCTTTTCATCATTTGGCTTAATTGGCTGTGCCACAATCCGG 231
Db 61 IleAlaAlaGlyValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
QY 232 GAAAGTCGCTGGAGCTGCGCAGTTTGTGTCATCTGCTTCTGCTTCTGCTTCTGCTG 291
Db 81 GluSerLysCysAlaLeuValThrPhePheIleLeuLeuIlePheIleAlaGlu 100
QY 292 GTTGTGTAGTGTGTTTGGATATGTTTACAGACCAAGGTGAAATGAGGTTCATCGC 351
Db 101 ValAlaAlaValAlaLeuValTyrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 AGCATTTCAGAAAGTGTATAGACCTACAATGGAACCAACCTGATGCTGCTAGCCGGCT 411
```

```

Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluAsp---PheThrGlnVal 139
QY 412 ATTGATTATGTACAGACAGACCTGATTTGTTGTTGGAATTACACTACTACTACAGTGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATACAGATTGGTTCAAGAAACCAAAACCCAGAGTGTCCCTCTTAGCTGCTGCAGAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysAsnAsp 177
QY 532 ACTCCAGCAAT-----TGTAATGGCAGCTGGCCACCCTTCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrGluGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGTGAGGCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATGATGCTG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
QY 637 ATCTGGGCGGCATCTGGCATTTCAGCTATTCAGCTGTGGGCATGCTGTGCTTGCATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTGTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 8
US-11-019-711-78
; Sequence 78, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsbrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corinne A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Perenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
```

; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; PRIOR APPLICATION NUMBER: 60/318,700
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 78
; LENGTH: 241
; TYPE: PR1
; ORGANISM: Homo sapiens
US-11-019-711-78

Alignment Scores:
Pred. No.: 2,12e-17 Length: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
DB: 7 Gaps: 6

US-10-608-388A-1 (1-759) x US-11-019-711-78 (1-241)
QY 7 CAGTGGGCATCCTCCAGACCGCTGCTGCTTTCTCAACCTCATCTTCTGGGG 66
Db 2 GlnCys---PheSerPheLeuLysThrMetMetLeuPheAsnLeuLeuLeuPheLeu 20
QY 67 GCAGCTGGCATTTATGCTATGTTGGGAGCCCTATGCTTTCATCTCACTATGATGACTATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyLletrpValSerIleaspGlyAlaSerPheLeu 40
QY 127 CACTTCTTGAAGATGTTACAGCTCATCCCTGCTGATG---ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGGAGCCCTTTTCATCATTTGGGCTAATTGGCTGCTGTCACAAATCCGG 231
Db 61 IleAlaAlaGlyValValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80-
QY 232 GAAAGTCGCTGTGACTTGCACGCTTTGTCTCATCTGCTGTTGTTTGTTCACAGAA 291
Db 81 GluSerLysCysAlaLeuValThrPhePhePheIleLeuLeuLeuPheIleAlaGlu 100
QY 292 GTTGTGTAGCTGTTTGGGATATGTTTACAGACCAAGTGGAATAGAGTTGATGCG 351
Db 101 ValAlaAlaAlaValValAlaLeuValTyrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 AGCATTCAGAAAGTATAGACCTACAAATGGAACCACTGATGCTGCTAGCCGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnGluasp---PheThrGlnVal 139
QY 412 ATTGATTATGACAGACAGCTGCTATGTTGTGGAAATTCACAACTACTCAGACTGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATACAGATTGTTTCAAGAAACCAAAACACAGAGTGCCTCTTAGCTGCTCAGAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177
QY 532 ACTGCCAGCAAT-----TGTAATGGCAGCGCTGCCCAACCTCCCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrLysGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLysThrAspIleargThrAsnAlaValThrVal 215
QY 637 ATCTGGGCGCGCACTGTCATTTGACAGTATTACGCTGCTGGCATGCTGTGCTGCATC 696

Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTCTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 9
US-11-234-786-114
; Sequence 114, Application US/11234786
; Publication No. US20060024301A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Dillon, Davin C.
; APPLICANT: Mitcham, Jennifer L.
; APPLICANT: Harlocker, Susan L.
; APPLICANT: Jiang, Yuqiu
; APPLICANT: Reed, Steven G.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Retter, Marc W.
; APPLICANT: Stolk, John A.
; APPLICANT: Day, Craig H.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.
; TITLE OF INVENTION: PROSTATE-SPECIFIC POLYPEPTIDES AND FUSION
; FILE REFERENCE: 210121.427C31
; CURRENT APPLICATION NUMBER: US/11/234,786
; CURRENT FILING DATE: 2005-09-23
; PRIOR APPLICATION NUMBER: US 09/568,857
; PRIOR FILING DATE: 2000-05-09
; PRIOR APPLICATION NUMBER: US 09/536,857
; PRIOR FILING DATE: 2000-05-27
; PRIOR APPLICATION NUMBER: US 09/483,672
; PRIOR FILING DATE: 2000-01-14
; PRIOR APPLICATION NUMBER: US 09/439,313
; PRIOR FILING DATE: 1999-11-12
; PRIOR APPLICATION NUMBER: US 09/352,616
; PRIOR FILING DATE: 1999-07-13
; PRIOR APPLICATION NUMBER: US 09/288,946
; PRIOR FILING DATE: 1999-04-09
; PRIOR APPLICATION NUMBER: US 09/232,149
; PRIOR FILING DATE: 1999-01-15
; PRIOR APPLICATION NUMBER: US 09/159,812
; PRIOR FILING DATE: 1998-09-23
; PRIOR APPLICATION NUMBER: US 09/115,453
; PRIOR FILING DATE: 1998-07-14
; PRIOR APPLICATION NUMBER: US 09/030,607
; PRIOR FILING DATE: 1998-02-25
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 701
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 114
; LENGTH: 241
; TYPE: PR1
; ORGANISM: Homo sapien
US-11-234-786-114

Alignment Scores:
Pred. No.: 2,12e-17 Length: 241
Score: 263.00 Matches: 68
Percent Similarity: 46.5% Conservative: 45
Best Local Similarity: 28.0% Mismatches: 114
Query Match: 18.4% Indels: 16
DB: 7 Gaps: 6

US-10-608-388A-1 (1-759) x US-11-234-786-114 (1-241)
QY 7 CAGTGGGCATCCTCCAGACCGCTGCTGCTTTCTCAACCTCATCTTCTGGGG 66

Db 2 GlnCys---PheSerPheIleLysThrMetMetIleLeuPheAsnLeuLeuPheLeu 20
QY 67 GCAGCTGGCAATTTATGCTATGGGAGCCTATGCTTCATCATCTATGATGAC 126
Db 21 CysGlyAlaAlaLeuLeuAlaValGlyIleTrpValSerIleAspGlyAlaSerPheLeu 40
QY 127 CACTTCTTTGAAGATGTGTACAGCTCATCCCTGCTGTAGTG-----ATC 171
Db 41 LysIlePheGlyProLeuSerSerSerAlaMetGlnPheValAsnValGlyTyrPheLeu 60
QY 172 ATAGCTGTAGGACCCCTGCTTTTCATCATTTGGCTAATTTGGCTGTGTGCCAATCCGG 231
Db 61 IleAlaAlaGlyValValPheAlaLeuGlyPheLeuGlyCysTyrGlyAlaLysThr 80
QY 232 GAAAGTGGTGGACTGCCAGCTTGTTCATCATCTGCTCTGCTTTGTTTGTACAGAA 291
Db 81 GluSerLysCysAlaLeuValThrPhePheIleLeuLeuLeuIlePheIleAlaGlu 100
QY 292 GTTGTGTAGTGTGTTGGGATATGTTTACAGAGCAAGGTGAAATGAGGTTCATCGC 351
Db 101 ValAlaAlaAlaValAlaLeuValTyrThrMetAlaGluHisPheLeuThrLeu 120
QY 352 AGCATTCAAGAAAGTGTATAAGACCTACATGAACCAACCCCTGCTGTAGCCGGCT 411
Db 121 LeuValValProAlaIleLysLysAspTyrGlySerGlnLysAsp---PheThrGlnVal 139
QY 412 ATTGATTATGACAGAGACAGCTGCTATGTTGGATTCAGAACTACTCATCAGCTGGAA 471
Db 140 TrpAsnThrThrMetLysGlyLeuLysCysGlyPheThrAsnTyrThrAspPheGlu 159
QY 472 AATCAGATGTGTCAAGAAACCAAAACCAAGAGTGTCCCTCTTAGCTGTGCGCAGAG 531
Db 160 AspSerProTyrPheLysGlu-----AsnSerAlaPheProPheCysCysAsnAsp 177
QY 532 ACTGCCAGCAAT-----TCTAATGGCAGCCTGGCCACCCCTTCCGACCTC 576
Db 178 AsnValThrAsnThrAlaAsnGluThrCysThrLysGlnLysAlaHis-----AspGln 195
QY 577 TATGCTGAGGGGTGTCAGGCTCTAGTAGTGAAGAGCTACAGAAATCATGATGATG 636
Db 196 LysValGluGlyCysPheAsnGlnLeuLeuTyrAspIleArgThrAsnAlaValThrVal 215
QY 637 ATCTGGCGCGCATGSCATTTGACGCTATTCAGCTGCTGGGATGCTGTGCTGTGCATC 696
Db 216 GlyGlyValAlaAlaGlyIleGlyGlyLeuGluLeuAlaAlaMetIleValSerMetTyr 235
QY 697 GTGTTGTGC 705
Db 236 LeuTyrCys 238

RESULT 10

US-11-108-172-1062

; Sequence 1062, Application US/11108172

; Publication No. US20050260177A1

; GENERAL INFORMATION:

; APPLICANT: Xu, Jiangchun

; APPLICANT: Lodes, Michael J.

; APPLICANT: Secrist, Heather

; APPLICANT: Benson, Darin R.

; APPLICANT: Meagher, Madeleine Joy

; APPLICANT: Stolk, John A.

; APPLICANT: Wang, Tongtong

; APPLICANT: Jiang, Fuguo

; APPLICANT: Smith, Carole L.

; APPLICANT: King, Gordon E.

; APPLICANT: Wang, Aijun

; APPLICANT: Clapper, Jonathan D.

; APPLICANT: Skeiky, Yasir A. W.

; APPLICANT: Fanger, Gary R.

; APPLICANT: Vedvick, Thomas S.

; APPLICANT: Carter, Darrick

; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS

; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE

FILE REFERENCE: 210121.471C15
CURRENT APPLICATION NUMBER: US/11108,172
CURRENT FILING DATE: 2005-04-15
PRIOR APPLICATION NUMBER: US 10/025,380
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: US 09/922,217
PRIOR FILING DATE: 2001-08-03
PRIOR APPLICATION NUMBER: US 09/833,263
PRIOR FILING DATE: 2001-04-10
PRIOR APPLICATION NUMBER: US 09/649,811
PRIOR FILING DATE: 2000-08-28
PRIOR APPLICATION NUMBER: US 09/609,448
PRIOR FILING DATE: 2000-06-29
PRIOR APPLICATION NUMBER: US 09/575,251
PRIOR FILING DATE: 2000-05-19
PRIOR APPLICATION NUMBER: US 09/519,444
PRIOR FILING DATE: 2000-03-06
PRIOR APPLICATION NUMBER: US 09/504,629
PRIOR FILING DATE: 2000-02-15
PRIOR APPLICATION NUMBER: US 09/480,321
PRIOR FILING DATE: 2000-01-10
PRIOR APPLICATION NUMBER: US 09/476,296
PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1130
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 1062
LENGTH: 237
TYPE: PRT
ORGANISM: Homo sapiens
US-11-108-172-1062

Alignment Scores:

Pred. No.:	2,99e-16	Length:	237
Score:	251.00	Matches:	66
Percent Similarity:	49.6%	Conservative:	48
Best Local Similarity:	28.7%	Mismatches:	94
Query Match:	17.6%	Indels:	22
DB:	7	Gaps:	8

US-10-608-388A-1 (1-759) x US-11-108-172-1062 (1-237)

QY	49	AACCTCATCTTCTGGGGGAGCTGGCAATTTATGCTATGTTGGGAGCCTATCTTCTATC	108
Db	16	AsnPheLeuPheTrpLeuCysGlyIleLeuAlaLeuAlaIleTrpValArgVal	35
QY	109	ACTTATGATGACTATGACCACCTTC---TTTGAAGATGTG-----TACAGCTCATCCT	159
Db	36	SerAsnAspSerGlnAlaIlePheGlySerGluAspValGlySerSerTyrValAla	55
QY	160	GCTGTAGTATCATGATGCTAGGAGCCTGCTTTTTCATCATTTGGGCTAATTTGGTGTCT	219
Db	56	ValAspIleLeuIleAlaValGlyAlaIleIleMetIleLeuGlyPheLeuGlyCysCys	75
QY	220	GCCACAATCCGGGAAGTCGCTGTGGACTGCCAGTTTGTGCATCATCTGCTCTTGTGT	279
Db	76	GlyAlaIleLysGluSerArgCysMetLeuLeuPhePheIleGlyLeuLeuLeuIle	95
QY	280	TTTGTACAGAAAGTTGTTGTAGTGGTTTGGATATGTTTACAGACCAAGGTGGAAAT	339
Db	96	LeuLeuLeuGlnValAlaThrGlyIleLeuGlyAlaValPheLysSerLysSerArg	115
QY	340	GAGGTTGATCGCAGCATTCAGAAAGTGTATAGACCTACAATGGAACCAACCTGATGCT	399
Db	116	IleValAsnGluThrLeuTyrGluAsnThrLysLeuLeuSerAlaThrGlyGluSerGlu	135
QY	400	GCT-----AGCCGGGCTATTGATTATGTACAGACAGCTGCATTTGTGTGGAATTCAC	453
Db	136	LysGlnPheGlnGluAlaIleIleValPheGlnGluPheLysCysGlyLeuVal	155
QY	454	AAC---TACTCAGACTGGGAAATATACAGATTGGTTTCAAGAAACCAACCAAGAGTGT	510
Db	156	AsnGlyAlaAlaAspTrpGlyAsn-----AsnPheGlnHisTyr	168


```

; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedwick, Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSTICS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1121
; LENGTH: 446
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1121

Alignment Scores:
Pred. No.: 3,15e-16 Length: 446
Score: 251.00 Matches: 66
Percent Similarity: 49.6% Conservative: 48
Best Local Similarity: 28.7% Mismatches: 94
Query Match: 17.6% Indels: 22
DB: Gaps: 8

US-10-608-388A-1 (1-759) x US-11-108-172-1121 (1-446)
QY 49 AACCTCATCTTCTGGGGGCGAGCTGTCATTTATGCTATGTTGGAGCCTATGCTTCATC 108
DB 219 AsnPheLeuPheTrpLeuCysGlyIleLeuLeuLeuAlaIleTrpValArgVal 238
QY 109 ACTTATGATGACTATGACCACTTC---TTTGAAGATGTG-----TACAGCTCATCCCT 159
DB 239 SerAsnAspSerGlnAlaIlePheGlySerGluAspValGlySerSerTrpValAla 258
QY 160 GCTGTAGTATGATGATGATGAGCCCTGCTTTTTCATCTGTTGGGCTAATGCTGCTGT 219
DB 259 ValAspIleLeuIleAlaValGlyAlaIleIleMetIleLeuGlyPheLeuGlyCysCys 278
QY 220 GCCAATCGGGAAGTGTGCTGTGACCTGACCTGTCACCTTGTCTATCTCTGCTCTGTT 279
DB 279 GlyAlaIleLysGluSerArgCysMetLeuLeuLeuPhePheIleGlyLeuLeuIle 298
QY 280 TTGTGCACAGAAGTGTGTAGTGGTGGTGGTATGTTTACAGACAAAGTGGAAAT 339
DB 299 LeuLeuLeuGlnValAlaThrGlyIleLeuGlyAlaValPheLysSerLysSerAspArg 318
QY 340 GAGTTGTAGCGACATTCAGAAAGTGTATACAGACCTTACAACTGGAACCAACCTGTGCT 399
DB 319 IleValAsnGluThrLeuTrpGluAsnThrLysLeuLeuSerAlaThrGlyGluSerGlu 338
```

```

QY 400 GCT-----AGCCGGCTATTGATTATGTACAGACAGACAGCTGCTATTGTTGCAATTCAC 453
DB 339 LysGlnPheGlnGluAlaIleValPheGlnGluGluPheLysCysCysGlyLeuVal 358
QY 454 AAC---TACTCAGACTGGGAAAATACAGATTGGTTTCAAAGAAACCAAAACACAGAGTGT 510
DB 359 AsnGlyAlaAlaAspTrpGlyAsn-----AsnPheGlnHisTyr 371
QY 511 CCTCTTAGCTGC---TGCAGAGAGACTGCCAGCAATTCG-----AATGGCAGCCTG 558
DB 372 ProGluLeuCysAlaCysLeuAspLysGlnArgProCysGlnSerTyrAsnGly----- 389
QY 559 GCCCACCCTTCGACCTCTATGCTGAGGGGTGTGAGGCTCTAGTAGTAGTGAAGAAGCTACAA 618
DB 390 -----LysGlnValTyrLysGluThrCysIleSerPheIleLysAspPheLeuAla 406
QY 619 GAATCATGATGATGATGATCTGGGCCGACATGGCGCATTTGCGATTTTACAGCTGCTGGGC 678
DB 407 LysAsnLeuIleIleValIleGlyIleSerPheGlyLeuAlaValIleGluIleLeuGly 426
QY 679 ATGCTGTGTGCTTGCATCGTGTGTGCAGA 708
DB 427 LeuValPheSerMetValLeuTrpCysGln 436

RESULT 13
US-11-019-711-80
; Sequence 80, Application US/11019711
; Publication No. US20060009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigar, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E
; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
```

```

; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 80
; LENGTH: 282
; TYPE: PRT
; ORGANISM: Caenorhabditis elegans
US-11-019-711-80

Alignment Scores:
Pred. No.: 3 398-16 Length: 282
Score: 250.50 Matches: 67
Percent Similarity: 41.5% Conservative: 50
Best Local Similarity: 23.8% Mismatches: 108
Query Match: 17.5% Indels: 57
DB: 7 Gaps: 11

US-10-608-388A-1 (1-759) x US-11-019-711-80 (1-282)
Qy 1 ATGGGCCAGTGGCGATCACCTCTCCAAAGACCGTGGTCTTTCTCAACCTCATCTTC 60
Db 1 MetGlySerCys---ValAsnAlaLeuArgIleValThrPheLeuPheAsnPheAlaPhe 19
Qy 61 TGGGGGGCAGCTGGCATTTATGCTATGTTGGAGCCCTATGCTTCATCCTCATCTATGATGAC 120
Db 20 Trp---LeuSerGlyValValPhe---GlyLeuGlyIleTrpLeuLeuPheAsnPro 37
Qy 121 TATGACCACCTCTTCTGAAGTGTGTACAGCTCATCTCTGCTGTA----- 165
Db 38 AlaAlaSerAspPhePheAlaLeuHisSerThrHisProGlyAlaPheArgTyrValGly 57
Qy 166 ---GTGATCATPAGCTAGGAGCCCTGCTTTTCATCATTTGGCTTAATGGCTGTGCC 222
Db 58 TrpPheLeuValGlyAlaGlyAlaIleIleIleLeuValGlyTyrPheGlyCysIleGly 77
Qy 223 ACAATCCGGGNAAGTCGTGGAGCTTCCACGTTTGTCTATCATCTCTGCTCTGCTTTT 282
Db 78 AlaTrpLysMetAsnGlnCysAlaLeuAlaPhePheCysCysIleLeuLeuAlaPhe 97
Qy 283 GTCACAGAAGTTGTTGTAGTGGTGTGGATGTTTACAGAGCAAGGTGGAAATGAG 342
Db 98 PheLeuGluLeuAlaAlaValThrLeuPheHisLysGlnGluHisIleLysHisTyr 117
Qy 343 GTTGATCGCAGCATTCAGAAGTGTATAAGACCTACAATGGA-----ACCAACCTGAT 396
Db 118 ValGluSerSer-----MetTyrAspThrIleArgAsnArgTyrSerSerGluThr 134
Qy 397 GCTGCTAGCCGGCTATTGATTATGTACAGAGAGCTGCATTTGTTGGAAATTCACAAC 456
Db 135 AlaPheLysAspAlaPheAspThrValGlnLulysPheGluCysCysGlyValLysThr 154
Qy 457 TACTCAGACTGGGAAATACAGATTGTTTCAAGAAACCAAAACCCAG----- 504
Db 155 TyrThrAspTrpLeuSerAlaArgTrpAspAlaGluProSerThrGlnLeuGluValAsn 174
Qy 504 ----- 504
Db 175 GluGluAspAlaGlyArgIleGluHisGlyIleGlyAlaPheGlyGlyAsnLysGlyThr 194
Qy 505 -----AGTGTCCCTTTAGTGTCTGCAGAGAGACTGCC-----AGC 540
Db 195 GlyTyrGlyArgValProSerSerCysCysAsnGluHisGlyLysLeuSerTyrProAsn 214
Qy 541 AATTTGTAATGGCAGCTGGCCAC---CCITCCACCTCTATGCTGAG----- 585
Db 215 AsnCysGlyArgSerPheSerGlnAlaProLeuAsnThrTyrAlaGlnPheIleAsnThr 234
Qy 586 ---GGGTGTGAGGCTCTAGTAGTGAAGAGCTACAAGAAATCATGATGATGATCTGG 642

```

```

Db 235 ArgGlyCysAlaAspAlaValTyrGluSerValSerSerLeuLeuValGly 254
Qy 643 GCAGCTGTCATTTGCAGCTATTCACCTGCTGGGCTG-----CTGTGT 687
Db 255 ValCysValValLeuCysIleValGlnLeuGlyIleValLeuSerMetThrLeuCys 274
Qy 688 GCTGC 693
Db 275 CysCys 276

RESULT 14
US-11-108-172-1085
; Sequence 1085, Application US/11108172
; Publication No. US20050260177A1
; GENERAL INFORMATION:
; APPLICANT: Xu, Jiangchun
; APPLICANT: Lodes, Michael J.
; APPLICANT: Secrist, Heather
; APPLICANT: Benson, Darin R.
; APPLICANT: Meagher, Madeleine Joy
; APPLICANT: Stolk, John A.
; APPLICANT: Wang, Tongtong
; APPLICANT: Jiang, Yugu
; APPLICANT: Smith, Carole L.
; APPLICANT: King, Gordon E.
; APPLICANT: Wang, Aijun
; APPLICANT: Clapper, Jonathan D.
; APPLICANT: Skeiky, Yasir A. W.
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick Thomas S.
; APPLICANT: Carter, Darrick
; TITLE OF INVENTION: COMPOUNDS FOR IMMUNOTHERAPY AND DIAGNOSIS
; TITLE OF INVENTION: OF COLON CANCER AND METHODS FOR THEIR USE
; FILE REFERENCE: 210121.471C15
; CURRENT APPLICATION NUMBER: US/11/108,172
; CURRENT FILING DATE: 2005-04-15
; PRIOR APPLICATION NUMBER: US 10/025,380
; PRIOR FILING DATE: 2001-12-19
; PRIOR APPLICATION NUMBER: US 09/922,217
; PRIOR FILING DATE: 2001-08-03
; PRIOR APPLICATION NUMBER: US 09/833,263
; PRIOR FILING DATE: 2001-04-10
; PRIOR APPLICATION NUMBER: US 09/649,811
; PRIOR FILING DATE: 2000-08-28
; PRIOR APPLICATION NUMBER: US 09/609,448
; PRIOR FILING DATE: 2000-06-29
; PRIOR APPLICATION NUMBER: US 09/575,251
; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: US 09/519,444
; PRIOR FILING DATE: 2000-03-06
; PRIOR APPLICATION NUMBER: US 09/504,629
; PRIOR FILING DATE: 2000-02-15
; PRIOR APPLICATION NUMBER: US 09/480,321
; PRIOR FILING DATE: 2000-01-10
; PRIOR APPLICATION NUMBER: US 09/476,296
; PRIOR FILING DATE: 1999-12-30
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1130
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1085
; LENGTH: 344
; TYPE: PRT
; ORGANISM: Homo sapiens
US-11-108-172-1085

Alignment Scores:
Pred. No.: 1 178-14 Length: 344
Score: 234.50 Matches: 60
Percent Similarity: 50.5% Conservative: 41
Best Local Similarity: 30.0% Mismatches: 78
Query Match: 16.4% Indels: 21
DB: 7 Gaps: 7

```

US-10-608-388A-1 (1-759) x US-11-108-172-1085 (1-344)

QY 136 GAAGATGTG-----TACAGCTCATCTCTGTGTAGTATGATCATGCTAGAGCCCTG 189
Db 153 GluapValGlySerSerSertyrValAlaValAspIleLeuAlaValGlyAlaIle 172
QY 190 CTTTTCATCTGGCTAATGGCTCTGTGCCAATCCGGGAAGTCGCTGTGACTT 249
Db 173 IleMetIleLeuGlyPheLeuGlyCysGlyAlaIleLeuSerArgCysMetLeu 192
QY 250 GCCACCTTTGTCTATCTCTCTCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 309
Db 193 LeuLeuPhePheIleGlyLeuLeuLeuIleLeuLeuGlnValAlaThrGlyIleLeu 212
QY 310 GGATATGTTTACAGACAAAGTGGAAATAGGTGTGTCGAGCATTCAGAAAGTGTAT 369
Db 213 GlyAlaValPheLeuSerSerArgGlyIleValAsnGluThrLeuTyrGluAsnThr 232
QY 370 AGACCTCAATGGAACCAACCTGATGCTGCT-----AGCCGGCTATTGATTATGTA 423
Db 233 LysLeuLeuSerAlaThrGlyGluSerGluGlnPheGlnGluAlaIleValPhe 252
QY 424 CAGAGACACTGCTATGTTGTGTGAATTCACAAC---TACTCAGACTGGGAAATACAGAT 480
Db 253 GlnGluGluPheLeuGlyCysGlyLeuValAsnGlyAlaAlaAspTrpGlyAsn----- 270
QY 481 TGGTTCAAGAAACCAAAACAGAGTGCCTCTTGTAGTGC---TGCAGAGAGACTGCC 537
Db 271 -----AsnPheGlnHisTyrProGluLeuCysAlaCysLeuAspLysGln 285
QY 538 ACCAATTGT-----AATGCACCTGGCCACCTCTCCGACCTCTATGCTGAGGG 588
Db 286 ArgProCysGlnSerTyrAsnGly-----LysGlnValTyrLysGluThr 300
QY 589 TGTGAGGCTCTAGTGTGAAGAGCTPACAGAAATCATGATCATGCTGTGCTGGCCGCA 648
Db 301 CysIleSerPheIleLeuAspPheLeuAlaLysAsnLeuIleIleValIleGlyIleSer 320
QY 649 CTGGCATTTCAGCTATTTCAGCTGTGCTGGGAGTCTGTGTGCTGTGCTGTGCTG 708
Db 321 PheGlyLeuAlaValIleGluIleLeuGlyLeuValPheSerMetValLeuTyrCysGln 340

RESULT 15
US-11-019-711-76
; Sequence 76, Application US/11019711
; Publication No. US2006009634A1
; GENERAL INFORMATION:
; APPLICANT: Kekuda, Ramesh
; APPLICANT: Alsobrook II, John P
; APPLICANT: Tchernev, Velizar T
; APPLICANT: Liu, Xiaohong
; APPLICANT: Spytek, Kimberly A
; APPLICANT: Patturajan, Meera
; APPLICANT: Grosse, William M
; APPLICANT: Lepley, Denise M
; APPLICANT: Burgess, Catherine E
; APPLICANT: Vernet, Corine A.M.
; APPLICANT: Li, Li
; APPLICANT: Gorman, Linda
; APPLICANT: Edinger, Shlomit R
; APPLICANT: Sciore, Paul
; APPLICANT: Ellerman, Karen
; APPLICANT: Malyankar, Uriel M
; APPLICANT: Rothenberg, Mark
; APPLICANT: Stone, David J
; APPLICANT: Boldog, Ferenc L
; APPLICANT: Guo, Xiaojia
; APPLICANT: Shenoy, Suresh G
; APPLICANT: Anderson, David W
; APPLICANT: Padigaru, Muralidhara
; APPLICANT: Taupier Jr, Raymond J
; APPLICANT: Miller, Charles E

; APPLICANT: Eisen, Andrew J
; TITLE OF INVENTION: Proteins and Nucleic Acids Encoding Same
; FILE REFERENCE: 21402-235
; CURRENT APPLICATION NUMBER: US/11/019,711
; CURRENT FILING DATE: 2004-12-21
; PRIOR APPLICATION NUMBER: US/10/037,417
; PRIOR FILING DATE: 2002-09-20
; PRIOR APPLICATION NUMBER: 60/260,018
; PRIOR FILING DATE: 2001-01-05
; PRIOR APPLICATION NUMBER: 60/260,360
; PRIOR FILING DATE: 2001-01-08
; PRIOR APPLICATION NUMBER: 60/272,411
; PRIOR FILING DATE: 2001-02-28
; PRIOR APPLICATION NUMBER: 60/272,817
; PRIOR FILING DATE: 2001-03-02
; PRIOR APPLICATION NUMBER: 60/291,186
; PRIOR FILING DATE: 2001-05-15
; PRIOR APPLICATION NUMBER: 60/303,231
; PRIOR FILING DATE: 2001-07-05
; PRIOR APPLICATION NUMBER: 60/305,060
; PRIOR FILING DATE: 2001-07-12
; PRIOR APPLICATION NUMBER: 60/318,405
; PRIOR FILING DATE: 2001-09-10
; PRIOR APPLICATION NUMBER: 60/318,700
; PRIOR FILING DATE: 2001-09-12
; NUMBER OF SEQ ID NOS: 227
; SOFTWARE: PatentIn, Ver. 2.1
; SEQ ID NO 76
; LENGTH: 240
; TYPE: PRT
; ORGANISM: Mus musculus
US-11-019-711-76

Alignment Scores:
Pred. No.: 4,79e-14 Length: 240
Score: 228.00 Matches: 64
Percent Similarity: 46.0% Conservative: 46
Best Local Similarity: 26.8% Mismatches: 107
Query Match: 16.0% Indels: 22
Ds: 7 Gaps: 7

US-10-608-388A-1 (1-759) x US-11-019-711-76 (1-240)

QY 28 AAGACCGTGTGCTTCTTCAACCTCATCTCTGGGGGCGAGCTGGCATTTTATGCTAT 87
Db 8 LysValMetMetPheLeuPheAsnLeuLeuPheLeuCysGlyAlaAlaLeuLeuAla 27
QY 88 GTGGAGCTATGTCTTTCATCATCTATGATGACCTATGACCTCTTTTGAAGATGTGTAC 147
Db 28 ValGlyIleTrpValSerValAspGlyThrSerPheLeuLysValPheGlySerLeuSer 47
QY 148 AGCTCATCTCTGCTGTAGTG-----ATCATAGCTGTAGGAGCCCTGCTT 192
Db 48 SerSerAlaMetGlnPheValAsnValGlyTyrPheLeuIleAlaAlaGlyAlaValLeu 67
QY 193 TTCATCTGGCTAAATGGCTGTGCTGCCAATCCGGGAAGTCGCTGTGAGCTTGC 252
Db 68 PheIleLeuGlyPheLeuGlyCysTyrGlyAlaHisSerGluAsnLysCysValLeuMet 87
QY 253 ACGTTTGTCTATCTCTCTTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGGA 312
Db 88 MetPhePheSerIleLeuLeuIlePheIleAlaGluIleAlaGlyAlaValValAla 107
QY 313 TATGTTTACAGACCAAGTGTGGAAT-----GAGTTGATCGCAGCATTCAG 360
Db 108 LeuValTyrThrLeuAlaGluGlnPheLeuThrLeuLeuValValProAlaIleGlu 127
QY 361 AAAGTGTATAAGACCTCAATGGAACCAACCTGCTAGCTAGCGGGCTATTGATTAT 420
Db 128 LysAspTyr-----GlyTyrGlnThrAsp---PheThrGlnValTrpAsnThr 142
QY 421 GTACAGACAGCTGCTATTTGTGTGGAATTCACACTACTCAGACTGGGAAATACAGAT 480
Db 421 GTACAGACAGCTGCTATTTGTGTGGAATTCACACTACTCAGACTGGGAAATACAGAT 480

Db 143 ThrMetGluGluLeuHisCysGlyPheAsnAsnTyrThrAspPheAsnAlaSerArg 162
Qy 481 TGGTTCAGAAGAACCAAAACCCAGAGTGTCCCTCTTAGCTGCTGC-----AGA 528
Db 163 PheValLysGlu-----AsnLysValPheProProCysCysAlaAsnProGlyAsn 180
Qy 529 GAGACTGCCAGCAATTGTAATGGCAGCCTGGCCACCCTTCGACCTCTATGCTGAGGGG 588
Db 181 HisThrValGluProCysThrGluGluLysAla-----LysSerMetLysValGlnGly 198
Qy 589 TGTGAGGCTCTAGTAGTGAAGAAGCTACAAGAAATCATGATGCATGTGATCTGGGCCGCA 648
Db 199 CysPheLysGluIleLeuHisArgIleArgAlaAsnAlaValThrValGlyGlyValAla 218
Qy 649 CTGGCATTTGCAGCTATTTCAGCTGCTGGGCATGCTGTGTGCTTGCATCGTGTGTGTC 705
Db 219 ValGlyValAlaAlaLeuGluLeuAlaAlaMetValValSerMetTyrLeuTyrCys 237

Search completed: April 4, 2006, 21:56:04
Job time : 23.5 secs

**This Page is Inserted by IFW Indexing and Scanning
Operations and is not part of the Official Record**

BEST AVAILABLE IMAGES

Defective images within this document are accurate representations of the original documents submitted by the applicant.

Defects in the images include but are not limited to the items checked:

☐ BLACK BORDERS

☒ IMAGE CUT OFF AT TOP, BOTTOM OR SIDES

☐ FADED TEXT OR DRAWING

☐ BLURRED OR ILLEGIBLE TEXT OR DRAWING

☐ SKEWED/SLANTED IMAGES

☐ COLOR OR BLACK AND WHITE PHOTOGRAPHS

☐ GRAY SCALE DOCUMENTS

☐ LINES OR MARKS ON ORIGINAL DOCUMENT

☒ REFERENCE(S) OR EXHIBIT(S) SUBMITTED ARE POOR QUALITY

☐ OTHER: _____

IMAGES ARE BEST AVAILABLE COPY.

As rescanning these documents will not correct the image problems checked, please do not report these problems to the IFW Image Problem Mailbox.